

DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF000008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00072; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA_1.
DR SMART; SM00001; EGF_like_1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLUTCARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 50.8%; Score 96; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 3.2e-09;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPFXXAEXIFRMXXRTROPFWSY 44
DB 41 ANSFEEFKKGNLERECMEETCSYEVEVRETFEDDKTKETWTKY 84

RESULT 7
ID 054740 PRELIMINARY; PRT; 481 AA.
AC 054740;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F410.
OS Mus musculus (Mouse).
OC Plasmod pluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00001; EGF_like_1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLUTCARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPFXXAEXIFRMXXRTROPFWSY 44
DB 41 ANSFEEFKKGNLERECMEETCSYEVEVRETFEDDKTKETWTKY 84

RESULT 8
ID 099132 PRELIMINARY; PRT; 481 AA.
AC 099132;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_I1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like_2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

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RT "Complete sequence of UC72A01."
CC Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AF318182; AK07918.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR MGD: MGI:97771; PROC.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 54.5%; Score 103; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLCSPXXAEXIFRXXXTROFWWSY 44
DB 42 ANSFLEMRPGSLERECMEICDLEBAQEIFQVVDTLAWIKY 85

RESULT 5
O9TR0 PRELIMINARY; PRT; 456 AA.
AC O9TR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunenberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
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DR EMBL: AJ001979; CA05126.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; signal.
FT SIGNAL 1 42
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
FT SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 52.9%; Score 100; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 5.5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLCSPXXAEXIFRXXXTROFWWSY 44
DB 43 ANSFLEIRAGSLERECMEICDFEAKEIFQVVDTLAWWSKY 86

RESULT 6
ID O63207 PRELIMINARY; PRT; 482 AA.
AC O63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S.,
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: X79807; CAA56202.1; -.
DR HSSP: P00742; IXKA.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match
Best Local Similarity 52.3%; Score 123; DB 4; Length 701;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAXEXIFRNXXRTQPFVSY 44
DB 61 ANAFLELRPGSLERCEKCEKCECFEEARELIFKQERTKLFWISY 104

RESULT 2
Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL EMBL; BC013896; AA113896.1; -.
DR MGD; MGI:97771; Proc.
DR INTERPRO; IPR000152; Asx_hydroxyl.
DR INTERPRO; IPR000561; EGF-like.
DR INTERPRO; IPR001881; EGF_Ca.
DR INTERPRO; IPR001254; Ser_protease_Try.
DR INTERPRO; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PROSITE; PS00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 011726568FCC274 CRC64;

Query Match
Best Local Similarity 45.5%; Score 109; DB 11; Length 460;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAXEXIFRNXXRTQPFVSY 44
DB 42 ANSFLERMPGSLERCEKCEKCECFEEARELIFQNEVDTLAFWIKY 85

RESULT 3
Q61109 PRELIMINARY; PRT; 446 AA.
AC Q61109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
DE F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino P.U.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; LEAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR INTERPRO; IPR002086; Aldehyde dehydr.
DR INTERPRO; IPR000152; Asx_hydroxyl.
DR INTERPRO; IPR001314; Chymotrypsin.
DR INTERPRO; IPR001064; Cystealin.
DR INTERPRO; IPR000561; EGF-like.
DR INTERPRO; IPR001881; EGF_Ca.
DR INTERPRO; IPR002383; GLA_blood.
DR INTERPRO; IPR001254; Ser_protease_Try.
DR INTERPRO; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00060; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match
Best Local Similarity 47.7%; Score 106; DB 11; Length 446;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAXEXIFRNXXRTQPFVSY 44
DB 42 ANSLEELMPGSLERCEKCEKCECFEEARELIFKSGERTKQFIWY 85

RESULT 4
Q99PC6 PRELIMINARY; PRT; 460 AA.
AC Q99PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
```

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10GLU28GLU_4
Perfect score: 189
Sequence: 1 ANGFLXXUREGSLXRXCRXX.....XXAEXIFRXRXTRQFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	65.1	701	4 Q96PQ8	Q96PQ8 homo sapien
2	109	57.7	460	11 Q91WN8	Q91WN8 mus musculu
3	106	56.1	446	11 Q61109	Q61109 mus musculu
4	103	54.5	460	11 Q93PC6	Q93PC6 mus musculu
5	100	52.9	456	6 Q91TR0	Q91TR0 canis fam11
6	96	50.8	482	11 Q63207	Q63207 rattus norv
7	93	49.2	481	11 Q54740	Q54740 mus musculu
8	93	49.2	481	11 Q99132	Q99132 mus musculu
9	93	49.2	481	11 Q88947	Q88947 mus musculu
10	90	47.6	456	6 Q14316	Q14316 homo sapien
11	90	47.6	461	6 Q95ND7	Q95ND7 pan troglod
12	90	47.6	461	6 Q95ND6	Q95ND6 pan troglod
13	89	47.1	469	6 Q9GMD9	Q9GMD9 ornithorhy
14	88	46.6	49	6 Q95ME8	Q95ME8 bos taurus
15	81	42.9	138	6 Q28894	Q28894 sus scrofa
16	80	42.3	433	13 Q90YK1	Q90YK1 brachydanio

17	78	41.3	100	4 Q15253	Q15253 homo sapien
18	77	40.7	608	13 Q9PTW7	Q9PTW7 struthio ca
19	77	40.7	648	6 Q29094	Q29094 sus scrofa
20	76	40.2	399	11 Q9CQW3	Q9CQW3 mus musculu
21	73.5	38.9	542	5 Q8TE13	Q8TE13 halocynthia
22	72	38.1	650	4 Q9NSD0	Q9NSD0 homo sapien
23	72	38.1	650	4 Q16519	Q16519 homo sapien
24	71	37.6	179	4 Q8TRA3	Q8TRA3 homo sapien
25	71	37.6	198	11 Q8RI82	Q8RI82 mus musculu
26	66	34.9	607	13 Q91001	Q91001 gallus gall
27	61	32.3	678	4 Q14393	Q14393 homo sapien
28	60	31.7	673	11 Q61592	Q61592 mus musculu
29	60	31.7	674	11 Q99K57	Q99K57 mus musculu
30	58	30.7	25	11 Q9QVH6	Q9QVH6 rattus sp.
31	58	30.7	674	11 Q63772	Q63772 rattus sp.
32	57	30.2	98	13 P82807	P82807 notechis sc
33	50.5	26.7	575	10 Q94E17	Q94E17 oryza sativ
34	50.5	26.7	608	10 Q9XF36	Q9XF36 medicago sa
35	50	26.5	472	13 Q98S05	Q98S05 gasteroste
36	50	26.5	613	13 Q98S06	Q98S06 gasteroste
37	50	26.5	910	13 Q98S07	Q98S07 gasteroste
38	49.5	26.2	196	10 Q04284	Q04284 selaginella
39	49.5	26.2	567	10 Q8W4J2	Q8W4J2 arabidopsis
40	49.5	26.2	603	10 Q91PC7	Q91PC7 arabidopsis
41	49.5	26.2	606	10 Q8SUG9	Q8SUG9 arabidopsis
42	49.5	26.2	651	10 Q8S218	Q8S218 oryza sativ
43	48.5	25.7	431	10 Q94EY5	Q94EY5 arabidopsis
44	48.5	25.7	492	10 Q9SMJ7	Q9SMJ7 cicor arlet
45	48.5	25.7	543	10 Q9MB23	Q9MB23 arabidopsis

ALIGNMENTS

RESULT 1
Q96PQ8 PRELIMINARY, PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocnjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AKS5686.1; -;
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT SITE 275 275 CHARGE RELAY SYSTEM.
FT ACT SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 48.7%; Score 92; DB 1; Length 492;
Best local Similarity 36.4%; Pred. No. 4.1e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXKRCXXLCSEFXAXEIPFNXXRTROQWVSY 44
Db 41 ANSFLFEVKGQNLRECELEBACSLSEAREVEFDAEQTDEFWSKY 84

RESULT 15
FA9 HUMAN STANDARD; PRT; 461 AA.
ID FA9 HUMAN STANDARD; PRT; 461 AA.
AC P00740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antithemophilic
RL factor B).";
RL Biochemistry 24:3736-3750(1985).
RN
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham U.B., Stadford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RT human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
RN
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Gianneli F., Gould K.G.,
RA Huddleston J.A., Brownlee G.G.;
RT "The gene structure of human anti-haemophilic factor IX.";
RL EMBO J. 3:1053-1060(1984).
RN
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=83220788; PubMed=6687940;
RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohli V.,
RA Finkel A., Tolstoshev P., Lecocq J.P.;
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
RT unique 52-base synthetic oligonucleotide probe deduced from the amino
RT acid sequence of bovine factor IX.";
RL Nucleic Acids Res. 11:2325-2335(1983).
RN
[5]
RP SEQUENCE OF 36-326 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=84300526; PubMed=6089157;
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
RT "Isolation and characterization of human factor IX cDNA:

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RT identification of Tag I polymorphism and regional assignment.";
RL Somatic. Cell Mol. Genet. 10:465-473(1984).
RN
[6]
RP SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE=88127096; PubMed=3340835;
RA Stoffet E.S., Koebert D.D., Sarkar G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing.";
RL Science 239:491-494(1988).
RN
[7]
RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE=94054330; PubMed=8236150;
RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN
[8]
RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
RX MEDLINE=90078229; PubMed=2592373;
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
RT chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN
[9]
RP HYDROXYLATION OF ASP-110.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN
[10]
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=78194509; PubMed=659613;
RA di Scipio R.G., Kurachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN
[11]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185715; PubMed=6425296;
RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
RL J. Biol. Chem. 259:5698-5704(1984).
RN
[12]
RP ERRATUM.
RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2583-2583(1985).
RN
[13]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=86189947; PubMed=3009023;
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
RT by mutation of arginine to glutamine at position -4.";
RL Cell 45:343-348(1986).
RN
[14]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN
[15]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).

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RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=7305314; PubMed=4264286;
 RA Titani K., Hemmerson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Tejleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1627084;
 RA Selander-Sunnehaugen M., Ullner M., Persson E., Tejleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnehaugen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trembelle J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).
 CC - FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC - CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC - SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC - PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC - PTM: N- AND O-GLYCOSYLATED.
 CC - PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC - MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X00673; CAA25286.1; -.
 CC PIR, A00925; EXBO.
 CC DR PDB, 1APO; 31-JAN-94.
 CC DR PDB, 1CCF; 31-MAY-94.
 CC DR PDB, 1WHE; 15-MAY-97.
 CC DR PDB, 1WHF; 15-MAY-97.
 CC DR MEROPS: S01.216; -.
 CC DR GlycositeDB: P00743; -.
 CC DR InterPro: IPR000152; Asx_hydroxyl.
 CC DR InterPro: IPR001314; Chymotrypsin.
 CC DR InterPro: IPR000561; EGF-like.
 CC DR InterPro: IPR000742; EGF 2.
 CC DR InterPro: IPR001881; EGF_Ca.
 CC DR InterPro: IPR002383; GLA_blood.
 CC DR InterPro: IPR001254; Ser_protease_Try.
 CC DR InterPro: IPR002944; VitK_dep_GLA.
 CC DR Pfam: PF00008; EGF; 2.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR Pfam: PF00594; gla; 1.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR PRINTS: PR00001; GLABLOOD.
 CC DR SMART: SM00179; EGF_CA; 1.
 CC DR SMART: SM00001; EGF_like; 1.
 CC DR SMART: SM00069; GLA; 1.
 CC DR SMART: SM00020; Tryp_Spc; 1.
 CC DR PROSITE: PS00010; Asx_HYDROXYL; 1.
 CC DR PROSITE: PS00022; EGF_1; 1.
 CC DR PROSITE: PS01186; EGF_2; 2.
 CC DR PROSITE: PS01187; EGF_CA; 1.
 CC DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
 CC KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC FT SIGNAL 1 23
 CC FT PROPEP 24 40
 CC FT CHAIN 41 180
 CC FT CHAIN 183 492
 CC FT PROPEP 183 233
 CC FT CHAIN 234 492
 CC FT PROPEP 476 492
 CC FT DOMAIN 86 122
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "protein C/vermont: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Suganara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandtille S., Vidard M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=931313192; PubMed=8324221;
 RA Gandtille S., Alhenc-Gelas M., Gausem P., Aillaud M.-F., Dupuy E.,
 RA Juhon-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; T-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertia R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Miller D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Glu domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous

RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrascu P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernard F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 QY
 Db 1 ANGFLXXLRGSLRXCRXXLCGFXXAEXIFRNXXRTQFW 41
 43 ANSFLELRHSLRRCIEBICDFEAKEIFQVVDTLAFW 83
 RESULT 14
 ID FA10 BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Pung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor)";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisilel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";

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FT  MOD_RES      69      69      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      72      72      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      75      75      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      79      79      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      103     103      SIMILARITY).
FT  MOD_RES      103     103      HYDROXYLATION (BY SIMILARITY).
FT  ACT_SITE     274     274      CHARGE RELAY SYSTEM.
FT  ACT_SITE     320     320      CHARGE RELAY SYSTEM.
FT  ACT_SITE     417     417      CHARGE RELAY SYSTEM.
FT  DISULFID     90      101      BY SIMILARITY.
FT  DISULFID     95      110      BY SIMILARITY.
FT  DISULFID     112     121      BY SIMILARITY.
FT  DISULFID     129     140      BY SIMILARITY.
FT  DISULFID     136     149      BY SIMILARITY.
FT  DISULFID     151     164      BY SIMILARITY.
FT  DISULFID     172     340      INTERCHAIN (BY SIMILARITY).
FT  DISULFID     239     244      BY SIMILARITY.
FT  DISULFID     259     275      BY SIMILARITY.
FT  DISULFID     368     402      BY SIMILARITY.
FT  DISULFID     413     441      BY SIMILARITY.
FT  CARBOHYD     61      61      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     187     187      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     205     205      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE      490 AA; 53965 MW; 3A39FA65AF2A6D11 CRC64;

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Query Match      49.7%; Score 94; DB 1; Length 490;
Best Local Similarity 38.6%; Pred. No. 1.8e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLEGGSLRXCRXXLCSPXXAEXIFRXXRTQFWVSY 44
Db 41 ANSFLEELKKGNLERECMEHCSEYEALEVFEDREKTNEMWNY 84

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RESULT 13

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PRTC_HUMAN      STANDARD; PRT; 461 AA.
ID P04070; O16001; O15190; O15189;
AC 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Aucoproteombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
CN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Sautter R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RN [3]
RA Nucleic Acids Res. 13:5233-5247(1985).
RP SEQUENCE FROM N.A.
RA MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).

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RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RA MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RA MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RN [7]
RA J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RA MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RN [8]
RA J. Biol. Chem. 267:5102-5107(1992).
RP 3D-STRUCTURE MODELING OF 175-450.
RA MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greenard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RN [9]
RA Protein Sci. 3:588-599(1994).
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RA MEDLINE=97157472; PubMed=9003757;
RA Wather T., Oganesyan V., Hof P., Huber R., Foundling S., Emon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RN [10]
RA EMBO J. 15:6822-6831(1996).
RP REVIEW ON PROC VARIANTS.
RA MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RN [11]
RA Thromb. Haemost. 69:77-84(1993).
RP VARIANT CYS-444.
RA MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RN [12]
RA Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RP VARIANT TRP-211 (LONDON-1).
RA MEDLINE=91329836; PubMed=2602169;
RA Grundy C.B., Chitcolle A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RN [13]
RA Nucleic Acids Res. 17:10513-10513(1989).
RP VARIANT CYS-272.
RA MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";

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FT PROPEP 32 40 FACTOR X LIGHT CHAIN.
FT CHAIN 41 179 FACTOR X HEAVY CHAIN.
FT CHAIN 183 488 ACTIVATION PEPTIDE.
FT PROPEP 183 234 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN 235 488 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 86 122 EGF-LIKE 2.
FT DOMAIN 125 488 SERINE PROTEASE.
FT DOMAIN 235 488 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 46 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 /FTID-CAR_000012.
FT CARBOHYD 231 231 /FTID-CAR_000013.
FT ACT_SITE 276 276 N-LINKED (GLCNAC. . .).
FT ACT_SITE 322 322 /FTID-CAR_000013.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.
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Query Match 50.8%; Score 96; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 7; Se-10;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXXREGSLKRCRXXLFXFXAEXIPIRNXXRTQFVWSY 44
41 ANSLLEMKKHLEHRECMETCSYBEAREVYEDSDKNEFWNKY 84

RESULT 12
FA10_RABIT STANDARD; PRT; 490 AA.
AC 019075;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; Pubmed=9101642;
RA Pendurthi U.R.; Anderson K.D.; James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.",
RL Thromb. Res. 85:503-514(1997).
CC CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
converts prothrombin to thrombin in the presence of factor Va,
calcium and phospholipid during blood clotting.
CC CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|Thr and then
Arg-|Ile bonds in prothrombin to form thrombin.
CC CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
MORE DISULFIDE BONDS.
CC CC -1- PTM: THE VITAMIN K-DEPENDENT ENZYMAIC CARBOXYLATION OF SOME
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CALCIUM (BY SIMILARITY).

CC CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
(BY SIMILARITY).
CC CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC CC -----
CC DR EMBL: AF003200; AB62542.1; -.
CC DR HSSP: P00742; IHCG.
CC DR MEROPS: S01.216; -.
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR001314; Chymotrypsin.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR000742; EGF 2.
CC DR InterPro: IPR001881; EGF_Ca.
CC DR InterPro: IPR002383; GLA_blood.
CC DR InterPro: IPR001254; Ser_protease_Try.
CC DR InterPro: IPR000294; Vitk_dep_GLA.
CC DR Pfam: PF00008; EGF_2.
CC DR Pfam: PF00089; trypsin; 1.
CC DR Pfam: PF00584; gla; 1.
CC DR PRINTS: PR00722; CHYMOTRYPSIN.
CC DR PRINTS: PR00001; GLABLOOD.
CC DR SMART: SM00179; EGF_CA; 1.
CC DR SMART: SM00001; EGF_like; 1.
CC DR SMART: SM00069; GLA; 1.
CC DR SMART: SM00020; Tryp_Spc; 1.
CC DR PROSITE: PS00010; ASX_HYDROXYL; 1.
CC DR PROSITE: PS00022; EGF_1; 1.
CC DR PROSITE: PS01186; EGF_2; 2.
CC DR PROSITE: PS01187; EGF_CA; 1.
CC DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC DR PROSITE: PS00240; TRYPSIN_DOM; 1.
CC DR PROSITE: PS00134; TRYPSIN_HIS; 1.
CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
CC KM Glycoprotein; Hydroxylase; Serine protease; Plasma; blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20
FT PROPEP 21 40
FT CHAIN 41 180
FT CHAIN 184 490
FT PROPEP 184 232
FT CHAIN 233 490
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 233 490
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 56 56
FT MOD_RES 59 59
FT MOD_RES 60 60
FT MOD_RES 65 65
FT MOD_RES 66 66

RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102 (1986).
 RP [3]
 RX SEQUENCE OF 13-488 FROM N.A.
 RA MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595 (1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314 (1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884 (1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702 (1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163 (1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.U., Hamsabhusnam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519 (1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Gardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966 (1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635 (1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; K03194; AAA52490.1; -;
 CC EMBL; M57285; AAA52421.1; -;
 CC EMBL; L29433; AAA52764.1; -;
 CC EMBL; L00390; AAA52764.1; JOINED.
 CC EMBL; L00391; AAA52764.1; JOINED.
 CC EMBL; L00382; AAA52764.1; JOINED.
 CC EMBL; L00393; AAA52764.1; JOINED.
 CC EMBL; L00394; AAA52764.1; JOINED.
 CC EMBL; L00395; AAA52764.1; JOINED.
 CC EMBL; L00396; AAA52764.1; JOINED.
 CC EMBL; M22613; AAA51984.1; -;
 CC EMBL; K01886; AAA52486.1; -;
 CC EMBL; M33297; AAA52636.1; -;
 CC PIR; A00924; EXHU.
 CC PIR; A25853; A25853.
 CC PIR; A24478; A24478.
 CC PDB; 1HCG; 08-MAY-95.
 CC PDB; 1FXV; 17-JUN-98.
 CC PDB; 1KXA; 23-MAR-99.
 CC PDB; 1XKB; 23-MAR-99.
 CC MEROPS; S01.216; -;
 CC GlycosSiteDB; P00742; -;
 CC GeneW; HGNC:3528; F10.
 CC MIM; 134530; -;
 CC MIM; 227600; -;
 CC InterPro; IPR000152; Asx hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR000742; EGF-2.
 CC InterPro; IPR001881; EGF-Ca.
 CC InterPro; IPR002383; GLA blood.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VltK_dep_GLA.
 CC Pfam; PF00089; trypsin; 1.
 CC Pfam; PF00594; gla; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC GlycoProtein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 CC SIGNAL 1 31
 CC POTENTIAL.

RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.E., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 domainless protein C."; J. Biol. Chem. 258:5548-5553(1983).
 RL J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 by Ca2+ binding to a high affinity site that does not contain gamma-
 carboxyglutamic acid."; J. Biol. Chem. 258:5554-5560(1983).
 RL J. Biol. Chem. 258:5554-5560(1983).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 SITE IS NECESSARY FOR THE RECOGNITION OF THE
 THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; K02435; AAA30685.1; -
 DR PIR; A00928; KXBO.
 DR HSSP; P04070; LPCU.
 DR MEROPS; S01.218; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TYP_Src; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PSS0134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT NON_TTR 1
 FT SIGNAL <1 29
 FT PROPEP 30 39

FT CHAIN 40 194
 FT CHAIN 197 456
 FT PEPTIDE 197 210
 FT DOMAIN 94 129
 FT DOMAIN 133 173
 FT DOMAIN 211 456
 FT MOD_RES 45 45
 FT MOD_RES 46 46
 FT MOD_RES 53 53
 FT MOD_RES 55 55
 FT MOD_RES 58 58
 FT MOD_RES 59 59
 FT MOD_RES 62 62
 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 110 110
 FT ACT_SITE 252 252
 FT ACT_SITE 298 298
 FT ACT_SITE 397 397
 FT DISULFID 56 61
 FT DISULFID 89 108
 FT DISULFID 98 103
 FT DISULFID 102 117
 FT DISULFID 119 128
 FT DISULFID 137 148
 FT DISULFID 144 157
 FT DISULFID 159 172
 FT DISULFID 180 318
 FT DISULFID 237 253
 FT DISULFID 368 382
 FT DISULFID 393 421
 FT CARBOHYD 136 136
 FT CARBOHYD 289 289
 FT CARBOHYD 350 350
 FT CARBOHYD 366 366
 FT VARIANT 82 82
 FT VARIANT 455 456
 FT CONFLICT 455 456
 SQ SEQUENCE 456 AA; 51407 MW; 6A9F6833F894C209 CRC64;
 Query Match 51.3%; Score 97; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 4.6e-10;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 Cy 1 ANGFLXLRGSLRXCRXXLCSPXXAEXIFRNXXRTQPFVSY 44
 Db 40 ANSTLELRPGNVRBESSEVCFEEAREIFQNTEDIMAFWSFY 83
 RESULT 11
 ID FA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340; 01, Created)
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stewart factor).
 GN F10.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 human coagulation factor X.";
 RL Gene 99:291-294(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=67026600; PubMed=3768336;

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-chromomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: AF191307; AAC28380.1; -.
 CC HSSP: P04070; 1PCU.
 CC MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 KW SIGNAL. 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67

FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT ACT_SITE 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CCL6D09 CRC64;
 Query Match 54.0%; Score 102; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 5.6e-11;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 OY 1 ANGFLXLLREGSLXRCXRLCSFXXAEXIFRNXXRTQRFWSY 44
 DB 42 ANSFLELRPSSLRCKEKTDFEAREIFONTENTMAFWSKY 85
 RESULT 10
 ID PRTC_BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic cleavage of the heavy chain of bovine protein C)
 DE factor XIV (Fragment).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
 RA "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RA Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RL [2]
 RP SEQUENCE OF 40-194.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RA "Amino acid sequence of the light chain of bovine protein C";
 RA J. Biol. Chem. 257:12170-12179(1982).
 RL [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RA "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RA Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RL [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RA "Amino acid sequence of the heavy chain of bovine protein C";
 RA J. Biol. Chem. 257:12180-12190(1982).
 RL


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DR PROSITE: PS00134; TRYPSIN_HIS; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 32
FT PROPEP 33 41
FT CHAIN 42 136
FT PEPTIDE 139 461
FT SITE 212 212
FT DOMAIN 96 131
FT DOMAIN 135 175
FT MOD_RES 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 254 254
FT ACT_SITE 300 300
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 105 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 320
FT DISULFID 239 255
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 215 215
FT CARBOHYD 291 291
FT CARBOHYD 355 355
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;

Query Match 57.1%; Score 108; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 4,4e-12;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRGSLRXRCXXLGFXXAEXLFRXXRTRPQWVSY 44
Db 42 ANSFLFVRAGSLRRCMEICDFEERQELFQVEDTLAWIKY 85

RESULT 7
FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964(1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U66079; AAC3796.1; -.
DR HSSP; P08709; 1BP9.
DR MEROPS; S01.215; -.
DR MGI: 109325; F7.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000284; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SMC0020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL; 1
FT PROPEP; 34
FT CHAIN; 42
FT CHAIN; 199
FT PEPTIDE; 199
FT SITE; 212
FT DOMAIN; 96
FT DOMAIN; 135
FT DOMAIN; 213
FT MOD_RES; 47
FT MOD_RES; 48
FT MOD_RES; 48
FT MOD_RES; 55
FT MOD_RES; 57
FT MOD_RES; 60
FT MOD_RES; 61
FT MOD_RES; 66
FT MOD_RES; 67
FT MOD_RES; 70
FT MOD_RES; 112
FT ACT_SITE; 253
FT ACT_SITE; 299
FT ACT_SITE; 402
FT DISULFID; 58
FT DISULFID; 91
FT DISULFID; 100
FT DISULFID; 104
FT DISULFID; 121
FT DISULFID; 139
FT DISULFID; 146
FT DISULFID; 161
FT DISULFID; 182
FT DISULFID; 238
FT DISULFID; 373
FT DISULFID; 398
FT CARBOHYD; 214
FT CARBOHYD; 290
FT CARBOHYD; 355
FT CONFLICT; 328
FT CONFLICT; 393
SQ SEQUENCE 461 AA; 51945 MW; 53FA0D5B194D5E CRC64;

Query Match 57.7%; Score 109; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 2.9e-12;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
Db 42 ANSFLXLRREGSLKRCXGXLCSPFXAXEIRNXXRTQFWVSY 44
1 ANGFLXLRREGSLKRCXGXLCSPFXAXEIRNXXRTQFWVSY 44
42 ANSFLXLRREGSLKRCXGXLCSPFXAXEIRNXXRTQFWVSY 44

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DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RC MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1331:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X64336; CAA45617.1; -.
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PR00008; EGF_2.
DR Pfam; PR00089; trypsin; 1.
DR Pfam; PF00594; Gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
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CC EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; 1CFH.
DR Genew; HGNC:9469; PRRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROSEP 1 20 POTENTIAL.
FT CHAIN 1 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 21 83 PROTEIN 1.
FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 24 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
Query Match 58.2%; Score 110; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 8.7e-13;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
OY 1 ANGFLXLRGSLXRCXKXLCSPXXAEXIFRNXXRTQFWVSY 44
DB 21 ANGFFEEIRQGNIERCKEFCFEERAEAFENNEKTKFWSY 64
RESULT 5
PRTC MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoprothombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
CN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;

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RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.O.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C."
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Hara M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS; CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-----
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CC or send an email to license@isb-sib.ch).
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CC EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; D43755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx hydroyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser protease TRY.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00059; GLA; 1.
DR SMART; SM00020; TRY; Spec. 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

```


RT [9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RP RX MEDLINE=99126538; PubMed=9925787;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RL inhibited with a Bp1 mutant.";
RN J. Mol. Biol. 285:2089-2104(1999).
RP [10] STRUCTURE BY NMR OF 105-145.
RX MEDLINE=96367502; PubMed=962950;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stefflo J.,
RT "Solution structure of the N-terminal EGF-like domain from human
RL factor VIIa.";
RN Biochemistry 37:10605-10615(1998).
RP [11] VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RT "Meade T.W., Tuddenham E.G.D.;
RA "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RL male.";
RN Blood 78:132-140(1991).
RP [12] VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patrarchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RL polymorphism in the factor VII gene (F7).";
RN Hum. Genet. 89:497-502(1992).
RP [13] VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patrarchini P., Reddelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RL (115His and 333Ser) in the human coagulation factor VII gene.";
RN Hum. Mol. Genet. 2:1055-1056(1993).
RP [14] VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kemballa-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RL coagulation factor VII.";
RN Hum. Mol. Genet. 2:1355-1359(1993).
RP [15] VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Chahng S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RL cleavage site for activation and altering binding to tissue factor.";
RN Blood 83:3524-3535(1994).
RP [16] VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Reddelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RL factors VII (294Ala-->Val) and X (333Ser-->Pro).";
RN Hum. Mol. Genet. 3:1175-1177(1994).
RP [17] VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
RA Suzuki K.;
RT "Factor VII Mle: homozygous asymptomatic type I deficiency caused by
an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
catalytic domain.";

RN	[Thromb. Haemost. 71:773-777(1994).]
RN	[18]
RP	VARIANT MET-419.
RX	MEDLINE=96247510; PubMed=8652821;
RA	Ardini A.A., Mannucci P.M., Bauer K.A.;
RT	"A Thrs39met mutation in factor VII of a patient with hereditary
RL	Blood 87:5085-5094(1996).
RN	[19]
RP	VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX	MEDLINE=97001216; PubMed=8844208;
RA	Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RT	Lungi B., Rodeghiero F., Marchetti G.;
RL	"Mutation pattern in clinically asymptomatic coagulation factor VII deficiency.";
RN	Hum. Mutat. 8:108-115(1996).
RN	[20]
RP	VARIANT VAL-304.
RX	MEDLINE=97037613; PubMed=8883260;
RA	Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA	Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
RA	Zazov R., Seltschik U.;
RT	"A1a244Val is a common, probably ancient mutation causing factor VII deficiency in Moroccan and Iranian Jews.";
RL	Thromb. Haemost. 76:283-291(1996).
RN	[21]
RP	VARIANTS MALTA THR-194 AND VAL-304.
RX	MEDLINE=98112461; PubMed=9452082;
RA	Alshinawi C., Secchi C., Galides R., Aquilina A., Felice A.E.;
RT	"Two new missense mutations (P134T and A244V) in the coagulation factor VII gene.";
RL	Hum. Mutat. Suppl. 1:S189-S191(1998).
CC	-I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIII, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC	-I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-- -lle bond in factor X to form factor xa.
CC	-I- SUBUNIT: HETERO-DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC	-I- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are produced by alternative splicing.
CC	-I- TISSUE SPECIFICITY: PLASMA.
CC	-I- PTM: THE VITAMIN K-DEPENDENT, ENZYMOLOGICAL CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC	-I- DISEASE: DEFECTS IN F7 CAN CAUSE CONJUGALOPATHY.
CC	-I- PHARMACEUTICAL: Available under the names Niasate or Novoseven (Novo Nordisk). Used for the treatment of bleeding episodes in
Query Match	65.1%; Score 123; DB 1; Length 466;
Best Local Similarity	52.3%; Pred.No.7.7e-15;
Matches 23; Conservative	5; Mismatches 16; Indels 0; Gaps 0,
Oy	1 ANGFLXLREGSLKRXCRXXLCSPFXAXEIPRNXKTRQFWVS 44 : : : : : : : : : : : : Db 61 ANAFLEBLRPGSLERECKECGCSFEAREBIFDARTRYLTWFMSY 104
RESULT 4	
TMGI_HUMAN	
ID _TMGI_HUMAN	STANDARD; PRT; 218 AA.
AC 014668;	
DT 15-JUN-2002 (Rel. 41, Created)	
DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein 1).	
DE PRG1 OR TMGI OR PRGP1.	
OS Homo sapiens (Human).	

```
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT DOMAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232
FT ACT_SITE 281
FT ACT_SITE 383
FT BINDING 377
FT DISULFID 56
FT DISULFID 89
FT DISULFID 94
FT DISULFID 111
FT DISULFID 130
FT DISULFID 137
FT DISULFID 151
FT DISULFID 166
FT DISULFID 174
FT DISULFID 198
FT DISULFID 217
FT DISULFID 233
FT DISULFID 349
FT DISULFID 379
FT MOD_RES 45
FT MOD_RES 46
FT MOD_RES 53
FT MOD_RES 55
FT MOD_RES 58
FT MOD_RES 59
FT MOD_RES 64
FT MOD_RES 65
FT MOD_RES 68
FT MOD_RES 74
FT MOD_RES 102
FT MOD_RES 121
FT CARBOHD 211
FT CARBOHD 242
FT CARBOHD 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 69.3%; Score 131; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.5e-16;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
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RESULT 3
ID PA7 HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DC 01-JAN-1988 (Rel. 06, Created)
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.",
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.",
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RL [3]
RN SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carlington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL [4]
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Tim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.",
RT Biochemistry 27:7785-7793(1988).
RL [5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Tim L., Wiberger F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.",
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.",
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.",
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.",
RL Nature 380:41-46(1996).
```

DR MEROPS; S01.215; -.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF-2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR001438; EGF-11.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001254; Ser protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0010; EGFBL00D.
 DR PRINTS; PRO0001; GLABLOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 DR liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 DR EGF-like domain; Repeat.
 FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
 FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 6 35 GLA-RICH.
 FT DOMAIN 87 128 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 153 407 EGF-LIKE 2.
 FT SITE 152 153 SERINE PROTEASE.
 FT ACT_SITE 193 193 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
 FT ACT_SITE 242 242 FACTOR IXA, OR THROMBIN).
 FT BINDING 338 338 BY SIMILARITY.
 FT BINDING 338 338 BY SIMILARITY.
 FT DISULFID 17 22 BY SIMILARITY.
 FT DISULFID 50 61 BY SIMILARITY.
 FT DISULFID 55 70 BY SIMILARITY.
 FT DISULFID 72 81 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 98 112 BY SIMILARITY.
 FT DISULFID 114 127 BY SIMILARITY.
 FT DISULFID 135 262 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT DISULFID 178 194 BY SIMILARITY.
 FT DISULFID 310 329 BY SIMILARITY.
 FT DISULFID 340 368 BY SIMILARITY.
 FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
 FT CARBOHYD 52 52 O-LINKED (GLC. . .).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

Query Match 76.8%; Score 149; DB 1; Length 407;
 Best Local Similarity 68.2%; Pred. No. 1,1e-19;
 Matches.. 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGLXRCXKXLSFXXAEXIFRNXXTRQFWISY 44
 Db 1 ANGLELLPGSLERCREELCSFEEAHEIFNEERTQFWISY 44

RESULT 2
 ID FA7_RABIT STANDARD; PRT; 444 AA.
 AC P98139; P79224;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93190306; PubMed=8383365;
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
 RT factor VII.";
 RL Thromb. Res. Suppl. 69:231-238(1993).
 RP [2]
 RN REVISION TO 395.
 RC TISSUE=Liver;
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSES. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to [license@isb-sid.ch](mailto:license@isb-sib.ch)).
 CC -----
 CC EMBL; U77477; AAB3326.1; -.
 CC HSP; P08709; IFAK.
 DR MEROPS; S01.215; -.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF-2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR001438; EGF-11.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001254; Ser protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10glu28glu_4
Perfect score: 189
Sequence: 1 ANGFLXLRBGLRXCRXX.....XAXEIXFNXXTRQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	78.8	407	FA7_BOVIN	P22457 bos taurus
2	131	69.3	444	FA7_RABIT	P98133 oryctolagus
3	123	65.1	466	FA7_HUMAN	P08709 homo sapien
4	110	58.2	218	TMG1_HUMAN	O14668 homo sapien
5	109	57.7	461	PRTC_MOUSE	P33587 mus musculu
6	108	57.1	461	PRTC_RAT	P31394 rattus norv
7	106	56.1	446	FA7_MOUSE	P70375 mus musculu
8	104	55.0	231	TMG3_HUMAN	O9b2d7 homo sapien
9	102	54.0	459	PRTC_PIG	O9g1p2 sus scrofa
10	97	51.3	456	PRTC_BOVIN	P00745 bos taurus
11	96	50.8	488	FA10_HUMAN	P00742 homo sapien
12	94	49.7	490	FA10_RABIT	O19045 oryctolagus
13	93	49.2	461	PRTC_HUMAN	P04070 homo sapien
14	92	48.7	492	FA10_BOVIN	P00743 bos taurus
15	90	47.6	461	FA9_BOVIN	P00740 homo sapien
16	88	46.6	416	FA9_HUMAN	P00741 bos taurus
17	86	45.5	458	PRTC_RABIT	O28661 oryctolagus
18	84	44.4	475	FA10_CHICK	P25155 gallus gall
19	83	43.9	452	FA9_MOUSE	P19540 canis fami
20	83	43.9	459	FA9_MOUSE	P16294 mus musculu
21	78	41.3	622	THRB_HUMAN	P00734 homo sapien
22	75	39.7	617	THRB_RAT	P18292 rattus norv
23	75	39.7	618	THRB_MOUSE	P19221 mus musculu
24	72	38.1	400	PRT2_HUMAN	P22891 homo sapien
25	72	38.1	649	PRTS_MACMU	O28820 macaca mula
26	72	38.1	675	PRTS_BOVIN	P07224 bos taurus
27	72	38.1	676	PRTS_HUMAN	P07225 homo sapien
28	71	37.6	202	TMG2_HUMAN	O14669 homo sapien
29	70	37.0	646	PRTS_RABIT	P98118 oryctolagus
30	69	36.5	226	TMG4_HUMAN	O9b2d6 homo sapien
31	69	36.5	376	FA10_TROCA	P81428 tropidichis
32	69	36.5	625	THRB_BOVIN	P00735 bos taurus
33	69	36.5	675	PRTS_RAT	P53813 rattus norv

34	68	36.0	396	1	PRT2_BOVIN	P00744 bos taurus
35	62	32.8	675	1	PRTS_MOUSE	O08761 mus musculu
36	56	29.6	413	1	NCPA_IHNV	P11298 infectious
37	53	28.0	604	1	VE1_BPV1	P03116 bovine pap
38	53	28.0	605	1	VE1_BPV1	P00772 saccharomy
39	43	22.8	484	1	SLT2_YEAST	P57612 buchnera ap
40	42	22.2	320	1	GSHB_BUCAI	P77493 escherichia
41	41	21.7	315	1	YDUB_ECOLI	P33697 thizobium m
42	41	21.7	348	1	EXOO_RHIME	P02678 petromyzon
43	41	21.7	477	1	FIBB_PETMA	O50864 myxococcus
44	41	21.7	1275	1	RFBC_MYXXA	P24280 saccharomyc
45	40	21.2	303	1	SCI4_YEAST	

ALIGNMENTS

RESULT 1	ID	FA7_BOVIN	STANDARD;	PRT;	407 AA.
AC	P22457;				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).				
GN	F7.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
NP	[1]				
RP	SEQUENCE.				
RX	MEDLINE=8908362; PubMed=3049594;				
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,				
RA	Iwanaga S.;				
RT	"Bovine factor VII. Its purification and complete amino acid				
RT	sequence.";				
RL	J. Biol. Chem. 263:14868-14877(1988).				
RL	[2]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.				
RX	MEDLINE=91344709; PubMed=2129367;				
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;				
RT	"A new trisaccharide sugar chain linked to a serine residue in the				
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";				
RT	Adv. Exp. Med. Biol. 281:121-131(1990).				
RL	-1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS				
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIa, FACTOR IXa, OR				
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR				
CC	AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa				
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO				
CC	FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.				
CC	-1- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to				
CC	form factor Xa.				
CC	-1- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED				
CC	BY A DISULFIDE BOND.				
CC	-1- TISSUE SPECIFICITY: PLASMA.				
CC	-1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME				
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND				
CC	CALCIUM.				
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
CC	-1- SIMILARITY: CONTRAINS 2 EGF-LIKE DOMAINS.				
DR	PIR; A31979; A31979.				
DR	HSPB; P08709; 1BP9.				

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A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-28/Domain: signal sequence #status predicted <Sig>
F:29-46/Domain: propeptide #status experimental <P>
F:31-91/Domain: Gla domain homology <Gla> light chain #status experimental <ALC>
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F:97-128/Domain: EGF homology <EGF>
F:134-170/Domain: EGF homology <EG2>
F:122-226/Domain: activation peptide #status experimental <ACT>
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:227-454/Domain: trypsin homology <TRY>
F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxylglutamic acid (Glu) #
F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
F:99/Binding site: carboxylate (Ser) (covalent) #status experimental
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental
F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 47.6%; Score 90; DB 1; Length 461;
Best Local Similarity 39.5%; Pred. No. 9.4e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRGSLKRXCRXXLCSPYXAEKIFRNXXRTROFWVS 44
Db 49 SGKLEEFVQGNLERCEKESFEAREVFENTERTTEFWKQY 91

RESULT 12

KFPBO
coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text_change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; TJ
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
A:Reference number: A14757; MUID:80056619; PMID:291916
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', '65-416 <KAT>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', '65-69 <MCM>
R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; MUID:82272386; PMID:6287289
A:Accession: I45891
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 52-139 <CHO>
A:Cross-references: GB:00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A:Reference number: A44556; MUID:69213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of a carboxylate covalently bound to Ser
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
C:Comment: The gamma-carboxylglutamic acid residues arise by posttranslational, vitamin K
C:Function: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stru
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-16/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <Gla>
F:51-82/Domain: EGF homology <EG1>
F:147-181/Domain: EGF homology <EG2>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxylglutamic acid (Glu) #sta
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide
F:53/Binding site: carboxylate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 46.6%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 1.9e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRGSLKRXCRXXLCSPYXAEKIFRNXXRTROFWVS 44
Db 3 SGKLEEFVQGNLERCEKESFEAREVFENTERTTEFWKQY 45

RESULT 13

EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence, revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SDB>
A:Cross-references: DDBJ:D00844; NID:g222869; PIDN:BA00724.1; PID:g222870
R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <GOT>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', '248-251, 'X', '253-261 <GOT>
A:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-40/Domain: propeptide #status predicted <P>
F:25-84/Domain: Gla domain homology <Gla>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:99-121/Domain: EGF homology <EG1>
F:122-226/Domain: EGF homology <EG2>
F:127-167/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #
F:57-62,90-101,99-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,4
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:196,207,228,285/Binding site: carboxylate (Asn) (covalent) #status predicted
F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 44.4%; Score 84; DB 1; Length 475;
Best Local Similarity 34.1%; Pred. No. 1.1e-06;

A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOZ>
R.McCrarw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A22673; MUID:85190593; PMID:3857619
A:Accession: A22673
A:Molecule type: mRNA
A:Residues: 1-193,'T',195-461 <MCG>
A:Cross-references: GB:M1309; NID:G180552; PIDN:AAA52023.1; PID:G180553
A>Note: the authors reported the codon ACA for residue 29 as Tyr
R.Jay, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstoch
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-b
A:Reference number: A21337; MUID:83220788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193,'T',195-461 <JNY>
A:Cross-references: GB:J00137; NID:G182610; PIDN:AAA52763.1; PID:G182611
R.Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193,'T',195-326 <JAG>
A:Cross-references: GB:M35672
R.Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12,'S',14-73,'P',75-82,'K',84-203,'P',205-216,'G',218-298,'A',299-356,'R',
A:Cross-references: GB:J00136; NID:G182608; PIDN:AAA98726.1; PID:G182609
A:Experimental source: liver
R.Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; MUID:90194857; PMID:2316207
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52,'XX',55-60,'X',62,'XX',65 <THA>
R.McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109,'X',111-115 <MCW>
R.Ballard, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
Eur. J. Biochem. 172, 565-572, 1988
A:Title: Characterisation of two differently processed forms of human recombinant factor
A:Reference number: S02527; MUID:8816735; PMID:3280512
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAL>
A>Note: processed forms expressed in recombinant system
R.Allard, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien,
EMBO J. 9, 3295-3301, 1990
A:Title: Characterization of recombinant human factor IX expressed in transgenic mice an
A:Reference number: S12058; MUID:91006024; PMID:2209546
A:Accession: S12058
A:Molecule type: mRNA; protein
A:Residues: 1-68 <JAL>
A>Note: processed forms expressed in recombinant system
R.Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
EMBO J. 9, 475-480, 1990
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
A:Reference number: S12377; MUID:90151623; PMID:2406129
A:Accession: S12377
A:Molecule type: protein

A:Residues: 92-130 <HAN>
A>Note: NMR detection of calcium binding by domain expressed in recombinant system
R.de la Salle, C.; Charmanlier, J.L.; Baab, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
Thromb. Haemost. 70, 370-371, 1993
A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
A:Reference number: 159612; MUID:94054330; PMID:8236150
A:Accession: 159612
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 444-461 <RES>
A:Cross-references: GB:S66752; NID:G439773; PIDN:AA828588.1; PID:G439774
R.Stotler, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A:Title: Genomic amplification with transcript sequencing.
A:Reference number: 159529; MUID:88127096; PMID:3340835
A:Accession: 159529
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 290-359 <RE2>
A:Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623
R.Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
Biochemistry 33, 5167-5171, 1994
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
A:Reference number: A54255; MUID:94227047; PMID:8172892
A:Accession: A54255
A:Molecule type: protein
A:Residues: 'D',204,'X',206-211,'212','D',214,'X',216-221,'D' <AGA>
A>Note: the residues designated 'X' were determined to be threonine bound to carbohydrat
R.Di Sciipio, R.G.; Kurachi, K.; Davie, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A:Title: Activation of human factor IX (Christmas factor).
A:Reference number: A18483; MUID:78194509; PMID:659613
A:Contents: annotation; activation; active site; carbohydrate binding
R.McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
A:Reference number: A37569
A:Contents: annotation
A>Note: 194-Thr was also found
R.Morita, T.; Isaacs, B.S.; Bemon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
A:Reference number: A37543; MUID:84185715; PMID:6425296
A:Contents: annotation; calcium binding
R.Morita, T.; Isaacs, B.S.; Bemon, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A:Reference number: A37544
A:Contents: annotation; calcium binding, correction
R.Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
A:Reference number: A37545; MUID:86189947; PMID:3009023
A:Contents: annotation; signal sequence cleavage site
R.Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
J. Biol. Chem. 264, 21257-21265, 1989
A:Title: Blood clotting factor IX (BIM) Nagoya: subunitation of arginine 180 by tryptophan
A:Reference number: A30622; MUID:90078229; PMID:2592373
A:Contents: annotation; sequence of mutant BIM Nagoya
A>Note: carboxylation, glycosylation, and cleavage sites
R.Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
submitted to the Brookhaven Protein Data Bank, November 1991
A:Reference number: A51252; PDB:1IXA
A:Contents: annotation; conformation in yeast
A>Note: recombinant form expressed in yeast
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C:Genetics:
A:Gene: GDB:F9
A:Cross-references: GDB:119900; OMIM:306900
A:Map position: Xq27.1-Xq27.2
A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

Gene 84, 517-519, 1989

Article: Cloning and characterization of the 5' end (exon 1) of the gene encoding human

A:Reference number: J54051; MUID:90128299; PMID:2612918

A:Accession: J54051

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-23 <RES>

A:Cross-references: GB:M32297; NID:g183860; PID:AA52636.1; PID:g553330

J.Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bida

J. Mol. Biol. 232, 947-966, 1993

Article: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.

A:Reference number: A49458; MUID:93360277; PMID:8355279

A:Contents: annotation; X-ray crystallography, 2.2 angstroms

C:Comment: The two chains held together by one disulfide bond are formed from a single-or

C:Genetics: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or

A:Gene: GDB:F10

A:Cross-references: GDB:119890; OMT:227600

A:Map position: 13q34-13q34

A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1

A:Note: deficiency of this factor causes Stuart disease

C:Function:

A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami

F:1-73/Domain: signal sequence #status predicted <SIG>

F:24-40/Domain: propeptide #status predicted <PRO>

F:25-84/Domain: Gla domain homology <GLA>

F:41-179/Product: coagulation factor X light chain #status experimental <LCH>

F:90-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>

F:183-468/Product: coagulation factor X heavy chain #status experimental <HCH>

F:183-234/Domain: activation peptide #status experimental <APT>

F:235-468/Product: coagulation factor Xa heavy chain #status experimental <ACT>

F:235-462/Domain: trypsin homology <TRY>

F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #statu

F:57-62/Disulfide bonds: #status predicted

F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/

F:109/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119,211/Binding site: carbohydrate (Thr) (covalent) #status experimental

F:221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:234-235/Cleavage site: Arg-Tile (coagulation factor IXa, coagulation factor VIIa) #statu

F:276,332,419/Active site: His, Asp, Ser #status experimental

Query Match 50.8%; Score 96; DB 1; Length 488;

Best Local Similarity 36.4%; Pred. No. 8.8e-09;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRGSLXRCRXLCSPFYXAEIFPNXRTQFWVS Y 44

Db 41 ANSFLEMKKGLHRECMETCTSYEARREVFEDSDKTMEFNK Y 84

RESULT 9

KXHU

prolein C (activated) (EC 3.4.21.69) precursor - human

N.Alternate names: autoprothrombin IIA; plasma protein C

C.Species: Homo sapiens (man)

C.Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text change 16-Jul-1999

C:Accession: A22331; A25426; A21781; A23789; A00927

R.Foster, D.C.; Yoshitake, S.; Davis, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A:Title: The nucleotide sequence of the gene for human protein C.

A:Reference number: A22331; MUID:85270390; PMID:2991887

A:Accession: A22331

A:Molecule type: DNA

A:Residues: 1-461 <FOS1>

A:Cross-references: GB:M11228; NID:g190333; PID:AAA60166.1; PID:g190334

R.Plutsky, J.; Hoskins, J.A.; Long, G.L.; Creditree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

Article: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471

A.Accession: A25426
 A.Molecule type: DNA
 A.Residues: 1-445, 'L', 446-461 <PLU>
 A.Cross-references: GB:M2712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R.Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A.Title: Characterization of a cDNA coding for human protein C.
 A.Reference number: A21781; MUID:84272714; PMID:6589623
 A.Accession: A21781
 A.Molecule type: mRNA
 A.Residues: 'Q', 107-461 <F082>
 A.Cross-references: GB:K02059; NID:g190332; PIDN:AAA60164.1; PID:g190333
 R.Beckmann, R.U.; Schmidt, R.U.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A.Title: The structure and evolution of a 461 amino acid human protein C precursor and
 A.Reference number: A23789; MUID:85269639; PMID:2991859
 A.Accession: A23789
 A.Molecule type: mRNA
 A.Residues: 1-461 <BBC>
 A.Cross-references: GB:Q02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R.Mileich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A.Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m
 A.Reference number: A44605; MUID:50293094; PMID:1694179
 A.Contents: annotation; carbohydrate binding sites; activation peptide
 A.Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R.Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A.Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A.Reference number: A44606; MUID:52184750; PMID:1544894
 A.Contents: annotation; beta-hydroxyaspartic acid
 C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 lyation of factor Va is strongly enhanced by complexing with protein S. Protein C also f
 C.Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.
 C.Genetics:
 A.Gene: GDB:PROC
 A.Cross-references: GDB:120317; OMIM:176860
 A.Map position: 2q13-2q21
 A.Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C.Superfamily: coagulant; factor X; EGF homology; Gla domain homology; trypsin homology
 C.Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F.1-32/Domain: signal sequence #status predicted <SIG>
 F.27-86/Domain: Gla domain homology <GLA>
 F.33-42/Domain: propeptide #status predicted <PRO>
 F.43-197/Product: protein C light chain #status predicted <LCH>
 F.92-131/Domain: EGF homology <EG1>
 F.140-175/Domain: EGF homology <EG2>
 F.200-461/Product: protein C heavy chain #status predicted <HCH>
 F.200-211/Domain: activation peptide #status experimental <APT>
 F.212-445/Domain: trypsin homology <TRY>
 F.48, 49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F.59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/D
 F.106-111/Dsulfide bond: #status predicted
 F.110/Binding site: carboxylate (Thr) (covalent) #status absent
 F.113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F.139, 290, 355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F.211-232/Cleavage site: Arg-Leu (thrombin) #status experimental
 F.253, 259, 402/Active site: His, Asp, Ser #status predicted
 F.371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #ext_change 08-Dec-2000
 C/Accession: S49075; J04670; PS0191; PS0190; 162745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 N/Note: Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra-
 A/Reference number: A58498; MUID:96093366; PMID:8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA1>
 A/Cross-references: EMBL:X79807; NID:g506600; PIDN:CAAS6202.1; PID:g506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; MUID:96194815; PMID:8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL:X79807; NID:g506600; PIDN:CAAS6202.1; PID:g506601
 A/Experimental source: Cos-1 cell
 R/Enyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
 A/Reference number: PS0190; MUID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: protein
 A/Residues: 41-56, 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Nihou, Y.
 Eur. J. Hematol. 52, 162-168, 1994
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: 146196; MUID:94222160; PMID:8168596
 A/Accession: 162745
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455396
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-40/Domain: propeptide #status predicted <PRO>
 F/25-84/Domain: Gla domain homology <GLA>
 F/41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F/90-121/Domain: EGF homology <EGF>
 F/129-164/Domain: EGF homology <EG2>
 F/183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F/183-231/Domain: activation peptide #status predicted <APT>
 F/232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F/232-460/Domain: trypsin homology <TRY>
 F/46-74, 54-56, 59, 60, 65, 66, 69, 72, 77/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F/57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 411
 F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F/187/Binding site: carboxylate (Asn) (covalent) #status experimental
 F/208/Binding site: carboxylate (Thr) (covalent) #status predicted
 F/218/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status
 F/274, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match 50.8%; Score 96; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 8, 7e-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBSGLKXRCXXKXICSEFXAXEIRNXXRTGPFVNSV 44
 DB 41 ANSFEEITKGNLEKRECEVEICSEFEAREVDFDNKTETFMVKY 84

RESULT 8

EXHU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N/Alternate names: Stuart factor
 C/Species: Homo sapiens (man)
 C/Date: 15-Nov-1984 #sequence revision 02-May-1994 #ext_change 08-Dec-2000
 C/Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00
 R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A/Title: Gene for human factor X: a blood coagulation factor whose gene organization is
 A/Reference number: A24478; MUID:87026600; PMID:3768336
 A/Accession: A24478
 A/Molecule type: DNA
 A/Residues: 1-488 <LEY>
 A/Cross-references: GB:I29433; GB:M14327; NID:g459809; PIDN:AAAS2764.1; PID:g182831
 A/Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation
 A/Reference number: J00917; MUID:91216473; PMID:1902434
 A/Accession: J00917
 A/Molecule type: mRNA
 A/Residues: 1-488 <MES>
 A/Cross-references: GB:M57285; NID:g182389; PIDN:AAAS2421.1; PID:g182390
 R/Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation
 A/Reference number: A42485; MUID:92218390; PMID:1313796
 A/Accession: A42485
 A/Molecule type: DNA
 A/Residues: 1-15 <MIA>
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A/Reference number: A25853; MUID:86221713; PMID:3011603
 A/Accession: A25853
 A/Molecule type: mRNA
 A/Residues: 19-284, 'E', 289-488 <KAU>
 A/Cross-references: GB:M2613; NID:g180335; PIDN:AAAS1984.1; PID:g180336
 R/Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A/Title: Characterization of an almost full-length cDNA coding for human blood coagulation
 A/Reference number: A22208; MUID:85216545; PMID:2582420
 A/Accession: A22208
 A/Molecule type: mRNA
 A/Residues: 13-441, 'S', 443-488 <FUN>
 A/Cross-references: GB:K03194; NID:g182840; PIDN:AAAS2490.1; PID:g182841
 R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A/Title: Characterization of a cDNA coding for human factor X.
 A/Reference number: A21284; MUID:84222026; PMID:6587384
 A/Accession: A21284
 A/Molecule type: mRNA
 A/Residues: 13-284, 'E', 289-488 <LEY>
 A/Cross-references: GB:K01886
 R/MOMLUN, B.A.; Fujikawa, K.; Kistiel, W.; Sasaagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss
 Biochemistry 22, 2875-2884, 1983
 A/Title: Complete amino acid sequence of the light chain of human blood coagulation factor
 A/Reference number: A20362; MUID:83257207; PMID:6671167
 A/Accession: A20362
 A/Molecule type: protein
 A/Residues: 41-179 <MCM>
 R/Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39415
 A/Molecule type: protein
 A/Residues: 183-234 <INO>
 A/Note: glycosylation sites
 A/Note: identification and characterization of beta-hydroxyaspartic acid
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.

```

F:121-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-191,238-254,373-387,398-426/Disulfide bonds: #stat
F:214,290,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F:251,299,402/Active site: His, Asp, Ser #status predicted

Query Match          57.7%; Score 109; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 4,4e-11;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXLLREGSLRXRCRXKXCSFXKXKXIFRNXXRTROFWWSY 44
Db 42 ANSFLEBNRPGSLRRCMEICDFEFAQRI FQVVEDTLAFWIKY 85

RESULT 5
518994
Protein C (activated) (EC 3.4.21.69) precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C/Accession: S18994; S24312
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A/Description: The cDNA cloning and mRNA expression of rat protein C.
A/Reference number: S24312; MUID:92329550; PMID:1627650
A/Accession: S24312
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-461 <OKA>
A/Cross-references: EMBL:X64336; NID:g556963; PIDN:CAA45617.1; PID:g556963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1331, 329-332, 1992
A/Title: The cDNA cloning and mRNA expression of rat protein C.
A/Reference number: S24312; MUID:92329550; PMID:1627650
A/Accession: S24312
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-461 <OKA>
A/Cross-references: EMBL:X64336; NID:g556963; PIDN:CAA45617.1; PID:g556963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1331, 329-332, 1992
A/Title: The cDNA cloning and mRNA expression of rat protein C.
A/Reference number: S24312; MUID:92329550; PMID:1627650
A/Accession: S24312
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-461 <OKA>
A/Cross-references: EMBL:X64336; NID:g556963; PIDN:CAA45617.1; PID:g556963
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:127-85/Domain: Gla domain homology <GUA>
F:133-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PC>
F:91-130/Domain: EGF homology <EG1>
F:113-174/Domain: EGF homology <EG2>
F:213-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-191,238-255,373-387,398-426/Disulfide bonds: #stat
F:214,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F:251,300,402/Active site: His, Asp, Ser #status predicted

Query Match          57.1%; Score 108; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 6,6e-11;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXLLREGSLRXRCRXKXCSFXKXKXIFRNXXRTROFWWSY 44
Db 42 ANSFLEBNRPGSLRRCMEICDFEFAQRI FQVVEDTLAFWIKY 85

RESULT 6
KXBO
protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N/Alternate names: autoprothrombin IIA; plasma protein C
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C/Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

```

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A/Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A/Reference number: A26250; MUID:85014626; PMID:6091100
A/Accession: A26250
A/Molecule type: mRNA
A/Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A/Title: Amino acid sequence of the light chain of bovine protein C.
A/Reference number: A18385; MUID:83007325; PMID:6896876
A/Accession: A18385
A/Molecule type: protein
A/Residues: 40-194 <FER>
A/Note: 82-Lys was also found
R:Dirksenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A/Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A/Reference number: A19316; MUID:83169769; PMID:6572939
A/Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
U. Biol. Chem. 257, 12180-12190, 1982
A/Title: Amino acid sequence of the heavy chain of bovine protein C.
A/Reference number: A18386; MUID:83007326; PMID:6896877
A/Accession: A18386
A/Molecule type: protein
A/Residues: 197-454, 'PV' <STR>
R:Bomon, N.L.; Debault, L.E.; Bomon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A/Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p
A/Reference number: A37541; MUID:83213513; PMID:6304092
A/Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Bomon, N.L.; Lane, T.M.; Bomon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A/Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A/Reference number: A37542; MUID:83213514; PMID:6406503
A/Contents: annotation; activation; calcium binding
C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B.
C/Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
cognition of the thrombin-thrombomodulin complex.
C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GUA>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EG1>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <AP>
F:211-440/Domain: trypsin homology <TRY>
F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,180-191,237-251,368-382,393-421/Disulfide bonds: #stat
F:136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match          51.3%; Score 97; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 5,5e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLLREGSLRXRCRXKXCSFXKXKXIFRNXXRTROFWWSY 44
Db 40 ANSFLELRPGVNRRCSEVCFEFAREIFONTDTJAFWFSFY 83

RESULT 7
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C/Species: Rattus norvegicus (Norway rat)

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignment)
145.545 Million cell updates/sec

Title: 10glu28glu_4

Perfect score: 189

Sequence: 1 ANGFLXKUREGSLKRXCRXX.....XXAEXIFRNXXRTQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	78.8	407	1 KFB07	coagulation factor
2	131	69.3	443	2 I46932	coagulation factor
3	123	65.1	466	1 KFHU7	coagulation factor
4	109	57.7	461	1 UK0210	protein C (activat
5	108	57.1	461	1 S18994	protein C (activat
6	97	51.3	456	1 KXBO	coagulation factor
7	96	50.8	482	1 EXRT	coagulation factor
8	96	50.8	488	1 EXHU	coagulation factor
9	93	49.2	461	1 KXHU	protein C (activat
10	92	49.7	492	1 EXBO	coagulation factor
11	90	47.6	461	1 KFHU	coagulation factor
12	88	46.6	416	1 KFB0	coagulation factor
13	84	44.4	475	1 EXCH	coagulation factor
14	83	43.9	452	1 A30351	coagulation factor
15	83	43.9	459	2 JU0419	coagulation factor
16	78	41.3	622	1 TBHU	thrombin (EC 3.4.2
17	77	40.7	642	1 S53433	thrombin (EC 3.4.2
18	75	39.7	617	2 S10511	thrombin (EC 3.4.2
19	75	39.7	618	2 A35827	thrombin (EC 3.4.2
20	72	38.1	422	1 KXHU	plasma protein 2 p
21	72	38.1	642	2 S53434	plasma protein 2 p
22	72	38.1	675	1 KXBO	plasma protein S p
23	72	38.1	676	1 KXHU	plasma protein S p
24	71	37.6	646	2 S38819	thrombin (EC 3.4.2
25	69	36.5	625	1 TXBO	thrombin (EC 3.4.2
26	69	36.5	625	1 KXRTS	plasma protein 2 p
27	68	36.0	296	1 KXBOZ	plasma protein 2 p
28	62	32.8	675	1 KXMS	plasma protein S p
29	61	32.3	678	2 B48089	growth arrest-spec

30	60	31.7	673	2 A48089	growth arrest-spec
31	58	30.7	674	2 I55476	growth potentialin
32	56	29.6	413	1 VHVNIH	nucleoprotein - in
33	53	28.0	605	1 W1WLB2	E1 protein - bovin
34	53	28.0	620	1 W1WLB2	E1 protein - bovin
35	49.5	26.2	594	2 D84859	probable MAP kinase
36	49.5	26.2	603	2 C96575	probable MAP kinase
37	48.5	25.7	576	2 G96763	probable MAP kinase
38	45.5	24.1	706	2 D86441	unknown protein (l
39	45	23.8	687	2 T08528	probable DNA topoi
40	44	23.3	267	2 JCI527	coat protein - pot
41	43	22.8	219	2 AE2449	hypothetical prote
42	43	22.8	484	2 S43737	protein kinase SUR
43	43	22.8	1101	2 T26919	hypothetical prote
44	43	22.8	1217	2 T21403	hypothetical prote
45	42.5	22.5	907	2 T15792	hypothetical prote

ALIGNMENTS

RESULT 1

KFB07
Coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-May-1990 #sequence revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Fujikawa, K.; Kistel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:83308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid

R:Haase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid

R:Haase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid

R:Haase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

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KM	Factor VIIA; human; shock heat treatment; protein stability;
KW	protein manufacture; protein conformation; mutant; mutain.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Active-site
FT	/note= "Member of the factor VIIA catalytic triad"
FT	Active-site
FT	/note= "Member of the factor VIIA catalytic triad"
FT	Active-site
FT	/note= "Member of the factor VIIA catalytic triad"
FT	Misc-difference
FT	344
FT	/label= Gly, Met, Thr
FT	/note= "Preferably Ala. wild type Ser"
XX	
PN	MO200177141-A1.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-DK00234.
XX	
PR	06-APR-2000; 2000DK-0000573.
BR	17-APR-2000; 2000US-197650P.
XX	
PA	(NOVO) NOVO NORDISK AS.
XX	
PI	Mathiesen F;
XX	
DR	WPI; 2001-657162/75.
PT	Stabilisation of a polypeptide e.g. in a pharmaceutical composition
PT	involves a shock heat treatment -
XX	
PS	Disclosure; Page -: 22pp; English.
XX	
CC	The invention describes a method of stabilising a polypeptide involving
CC	shock heat treatment of the polypeptide. The method is useful in a
CC	pharmaceutical composition, in the industrial or large scale method of
CC	manufacturing a polypeptide, also as a unit operation during preparation,
CC	purification, recovery and/or formulation of polypeptides. The shock heat
CC	treatment improves the protein stability without substantial loss of
CC	biological activity. The method can be applied to change polypeptide
CC	conformation in a very fast and non-invasive manner. The polypeptide
CC	formed is stable. The method is also useful for decreasing the
CC	association of the polypeptide. This sequence represents a modified
CC	human factor VIIA protein, mutated at the catalytic site, described
CC	in the invention.
CC	Note: This sequence does not appear in the specification but has
CC	been obtained using information given in the invention.
XX	
SEQ	Sequence 406 AA:
XX	
Query Match	65.1%; Score 123; DB 22; Length 406;
Best Local Similarity	52.3%; Pred.No. 1.le-11;
Matches 23; Conservative	5; Mismatches 16; Indels 0; Gaps 0;
OY	1 ANGFLXLAREGSIXRCRXKLCSPFXAAEIPFNXXKTROFWISY 44
DB	1 ANAFLELRPGSLERCKEEQCSFEFARBIFFDAERTKLFWISY 44
XX	
RESULT 14	
AAM52171	
ID	AAM52171 standard; Protein; 406 AA.
XX	
AC	AAM52171;
XX	
DT	07-FEB-2002 (first entry)
DE	Human FVII SEQ ID NO 1.
XX	

KW	Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KV	cardiac; hepatocytic; cerebroprotective; haemophilia; liver disease;
KM	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Misc-difference
FT	6
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	7
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	14
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	16
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	19
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	20
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	25
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	26
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	29
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	35
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	52
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference
FT	60
FT	/note= "O-glycosylated"
FT	
FT	Misc-difference
FT	145
FT	/note= "N-glycosylated"
FT	
FT	Misc-difference
FT	152..153
FT	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	
FT	Misc-difference
FT	322
FT	/note= "N-glycosylated"
XX	
PN	WO200158935-A2.
XX	
PD	16-AUG-2001.
XX	
PF	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
XX	
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaaes C;
XX	
DR	WPI; 2001-581807/65.
XX	
DR	N-PSDB; AA199982.
XX	
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -
XX	
PS	Claim 1; Page 81-83; 89pp; English.
XX	

[illegible]

XX	AC	AAK35764;
XX <th>DT</th> <th>24-SEP-1993 (first entry)</th>	DT	24-SEP-1993 (first entry)
XX <th>DE</th> <th>Factor VII (VII).</th>	DE	Factor VII (VII).
XX <th>KM</th> <th>PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;</th>	KM	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW <th>Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;</th>	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;	
XX <th>exosite; catalytic activity.</th>	exosite; catalytic activity.	
OS <th>Homo sapiens.</th>	Homo sapiens.	
XX <th>Key</th> <th>Location/Qualifiers</th>	Key	Location/Qualifiers
FT <th>Region</th> <th>1..152</th>	Region	1..152
FT <th>Region</th> <th>/note= "Factor VII light chain"</th>	Region	/note= "Factor VII light chain"
FT <th>Region</th> <th>153..406</th>	Region	153..406
FT <th>Peptide</th> <th>/note= "Factor VII heavy chain"</th>	Peptide	/note= "Factor VII heavy chain"
FT <th>Peptide</th> <th>374..388</th>	Peptide	374..388
FT <th>Peptide</th> <th>/note= "exosite 1"</th>	Peptide	/note= "exosite 1"
FT <th>Peptide</th> <th>290..310</th>	Peptide	290..310
FT <th>Peptide</th> <th>/note= "exosite 2"</th>	Peptide	/note= "exosite 2"
FT <th>Peptide</th> <th>290..310</th>	Peptide	290..310
FT <th>Peptide</th> <th>/note= "pref. PC polypeptide; claim 2, page 136"</th>	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"
FT <th>Peptide</th> <th>374..388</th>	Peptide	374..388
FT <th>Peptide</th> <th>/note= "pref. PC polypeptide; claim 2, page 136"</th>	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"
FT <th>Peptide</th> <th>289..304</th>	Peptide	289..304
FT <th>Peptide</th> <th>/note= "pref. PC polypeptide; claim 4, page 137"</th>	Peptide	/note= "pref. PC polypeptide; claim 4, page 137"
FT <th>Peptide</th> <th>290..304</th>	Peptide	290..304
FT <th>Peptide</th> <th>/note= "pref. PC polypeptide; claim 4, page 137"</th>	Peptide	/note= "pref. PC polypeptide; claim 4, page 137"
FT <th>Peptide</th> <th>245..266</th>	Peptide	245..266
FT <th>Peptide</th> <th>/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"</th>	Peptide	/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
XX <th>PN</th> <th>W09309804-A.</th>	PN	W09309804-A.
XX <th>PD</th> <th>27-MAY-1993.</th>	PD	27-MAY-1993.
XX <th>PE</th> <th>18-NOV-1992; 92MO-US10242.</th>	PE	18-NOV-1992; 92MO-US10242.
XX <th>PR</th> <th>18-NOV-1991; 91US-0793989.</th>	PR	18-NOV-1991; 91US-0793989.
XX <th>PA</th> <th>(SCRI) SCRIPPS RES INST.</th>	PA	(SCRI) SCRIPPS RES INST.
XX <th>PI</th> <th>Griffin JH, Masters RM;</th>	PI	Griffin JH, Masters RM;
XX <th>DR</th> <th>WPI; 1993-182244/22.</th>	DR	WPI; 1993-182244/22.
XX <th>PT</th> <th>Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples</th>	PT	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
XX <th>PS</th> <th>Disclosure; Page 133-135; 149pp; English.</th>	PS	Disclosure; Page 133-135; 149pp; English.
XX <th>CC</th> <th>The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood CC common. of 0.1-100 (pref. 0.5-10) microm.</th>	CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood CC common. of 0.1-100 (pref. 0.5-10) microm.
CC <th>NB:</th> <th>Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.</th>	NB:	Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
XX <th>Sequence</th> <th>406 AA;</th>	Sequence	406 AA;
XX <th>Query Match</th> <th>65.1%; Score 123; DB 14; Length 406;</th>	Query Match	65.1%; Score 123; DB 14; Length 406;
DB <th>Best Local Similarity</th> <th>52.3%; Pred. No. 1,le-11;</th>	Best Local Similarity	52.3%; Pred. No. 1,le-11;
Matches <th>23; Conservative</th> <th>5; Mismatches 16; Indels 0; Gaps 0;</th>	23; Conservative	5; Mismatches 16; Indels 0; Gaps 0;
0Y <th>1</th> <th>ANGFLXLRBGLXRXCRXXLCSFYXAXEIRFNXXRTROFWVSY 44</th>	1	ANGFLXLRBGLXRXCRXXLCSFYXAXEIRFNXXRTROFWVSY 44
DB <th>1</th> <th>ANAFLELRPGSLRECKEEOCSFEAREIFPDARRTKLFWISY 44</th>	1	ANAFLELRPGSLRECKEEOCSFEAREIFPDARRTKLFWISY 44

XX 29-APR-1999.
 XX 20-OCT-1996; 98WO-US22152.
 XX 23-OCT-1997; 97US-0955636.
 XX (MINU) UNIV MINNESOTA.
 XX Nelsestuen GL;
 XX WPI; 1999-288309/24.
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX Disclosure; Page 15; 86pp; English.
 XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX Sequence 44 AA;
 XX
 Query Match 65.1%; Score 123; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ANGLFLXLRREGSLXRCRXLLCSFXXAEXIFRNXXRTROFWVS 44
 DB 1 ANAFLLXXLRPGSLXRCXKXQCSFXXARXIFKDXRRTKLFWISY 44
 RESULT 7
 AAB36395
 ID AAB36395 standard; peptide; 44 AA.
 AC AAB36395;
 DT 27-FEB-2001 (first entry)
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX Homo sapiens.
 OS
 PN WO200066753-A2.
 PD 09-NOV-2000.
 XX 28-APR-2000; 2000WO-US11416.
 XX 29-APR-1999; 99US-0302239.
 XX (MINU) UNIV MINNESOTA.
 XX Nelsestuen GL;
 XX WPI; 2001-007226/01.
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified

PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX Disclosure; Page 12; 81pp; English.
 XX The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 XX Sequence 44 AA;
 XX
 Query Match 65.1%; Score 123; DB 22; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ANGLFLXLRREGSLXRCRXLLCSFXXAEXIFRNXXRTROFWVS 44
 DB 1 ANAFLLXXLRPGSLXRCXKXQCSFXXARXIFKDXRRTKLFWISY 44
 RESULT 8
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.
 AC AAB84870;
 DT 31-UTL-2001 (first entry)
 DE Mutant blood coagulant factor VII (FVII-31).
 XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 311..317
 FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX JP2001061479-A.
 PD 13-MAR-2001.
 XX 24-AUG-1999; 99JP-0237610.
 XX 24-AUG-1999; 99JP-0237610.
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 2001-310677/33.
 XX N-PSDB; AAH19463.
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX Claim 14; Page 20-21; 29pp; Japanese.
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

```

QY      1 ANGFLXLRREGSLXRRCRXKLCSPFXAAEXIFPNXXRTROFWWSY 44
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 ANAFLLXLRLREGSLXRXCCKXXCQCSFPXXARXIFXDARTKLFWISY 44

RESULT 4
AA18311
ID      AAY18311 standard; peptide; 44 AA.
AC      AAY18311;
DT      17-AUG-1999 (first entry)
DE      Modified GLA domain of vitamin K-dependent protein.
KW      GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
        therapy.
OS      Homo sapiens.
SC      Synthetic.
FA      Key Location/Qualifiers
FT      Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
        acid"
PD      WO920767-A1.
PE      29-APR-1999.
PF      20-OCT-1998; 98MO-US22152.
PR      23-OCT-1997; 97US-0955636.
PT      (MNU ) UNIV MINNESOTA.
PI      Nelsstuen GL;
DR      WPI; 1999-288309/24.
PC      Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
        acid domain, useful for treating clotting disorders
PS      Disclosure; Page 80; 86pp; English.
SQ      This sequence represents a modified GLA (gamma-carboxyglutamic acid)
        domain. The invention relates to a vitamin K-dependent polypeptide
        comprising a modified GLA domain containing an amino acid substitution
        which enhances membrane binding of the modified polypeptide as compared
        to the native polypeptide. The polypeptide is used to treat a clotting
        disorder by decreasing or increasing clot formation. Modification of the
        GLA domain results in a protein which has enhanced membrane binding
        affinity as compared to the native protein.
        Sequence 44 AA;

Query Match 56.7%; Score 126; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 4,3e-13;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY      1 ANGFLXLRREGSLXRRCRXKLCSPFXAAEXIFPNXXRTROFWWSY 44
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 ANAFLLXLRLREGSLXRXCCKXXCQCSFPXXARXIFXDARTKLFWISY 44

RESULT 5
AA18302
ID      AAY18302 standard; peptide; 44 AA.
AC      AAY18302;
DT      17-AUG-1999 (first entry)

```

DE		Modified GLA domain of vitamin K-dependent protein.
XX	KW	GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX	KM	therapy.
XX	OS	Homo sapiens.
OS	XX	Synthetic.
FH	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"	
FT		
PN	WO9920767-A1.	
XX	PD	
XX	PD	29-APR-1999.
XX	PF	20-OCT-1998; 98WO-US22152.
XX	PR	23-OCT-1997; 97US-0955636.
PA	(MINU) UNIV MINNESOTA.	
PI	Nelstuen GW;	
DR	WP1; 1999-288309/24.	
XX	PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT	acid domain, useful for treating clotting disorders	
PS	Claim 11; Page 81; 86pp; English.	
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid)	
CC	domain. The invention relates to a vitamin K-dependent polypeptide	
CC	comprising a modified GLA domain containing an amino acid substitution	
CC	which enhances membrane binding of the modified polypeptide as compared	
CC	to the native polypeptide. The polypeptide is used to treat a clotting	
CC	disorder by decreasing or increasing clot formation. Modification of the	
CC	GLA domain results in a protein which has enhanced membrane binding	
CC	affinity as compared to the native protein.	
SO	Sequence 44 AA:	
	Query Match 65.6%; Score 124; DB 20; Length 44;	
	Best Local Similarity 75.0%; Pred. No. 9.1e-13;	
	Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
OY	1 ANGFLXLREBSGLRXCRXXLCSFYXAEXIRNXXRTQFVVS Y 44	
	: : : : :	
DB	1 ANAFPLXLRQGSILRXCKXKOCSEFXAXRIFEDAKRYTLFWIS Y 44	
	: : : : :	
RESULT 6		
ID	AAI18305 standard; peptide; 44 AA.	
AC	AAI18305;	
DT	17-AUG-1999 (first entry)	
DE	Human factor VII GLA domain.	
XX	GLA domain; vitamin K-dependent protein; clotting disorder;	
KM	therapy.	
XX	Homo sapiens.	
OS		
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 1..44	
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"	
FT		
PN	WO9920767-A1	

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 15; 86pp; English.
 XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 82.5%; Score 156; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 6.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRGSLRXRCRXLCSPFXAEXIFRNXXRTQFWVSY 44
 DB 1 ANGFLXXLRGSLRXRCRXLCSPFXAHXIFRNXXRTQFWVSY 44
 XX
 RESULT 2
 ID AAB36396 standard; peptide; 44 AA.
 AC AAB36396;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
 XX
 KM Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KM factor X; prothrombin; enhanced membrane binding affinity;
 KM clot formation; thrombolytic; haemostatic; bleeding disorder;
 KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KM liver disease.
 XX
 OS Bos taurus.
 XX
 PN WO200066753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 PS WPI; 2001-007226/01.
 XX
 DR Novel vitamin K-dependent polypeptide useful for treating clotting
 XX disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity
 XX
 PS Disclosure; Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type bovine factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 82.5%; Score 156; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 6.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRGSLRXRCRXLCSPFXAEXIFRNXXRTQFWVSY 44
 DB 1 ANGFLXXLRGSLRXRCRXLCSPFXAHXIFRNXXRTQFWVSY 44
 XX
 RESULT 3
 ID AAY18310 standard; peptide; 44 AA.
 AC AAY18310;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note="Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 PN MO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 PS WPI; 1999-288309/24.
 XX
 DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 XX acid domain, useful for treating clotting disorders
 PT
 PT
 XX
 PS Disclosure; Page 80; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 68.3%; Score 129; DB 20; Length 44;
 Best Local Similarity 77.3%; Pred. No. 1.4e-13;
 Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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/ CURRENT APPLICATION NUMBER: US/10/132,829
/ CURRENT FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: 60/286,314
/ PRIOR FILING DATE: 2001-04-25
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 5
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          45.8%; Score 87; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRBSGLXRCXXKXLCSPXXAFKIFRNXXRTQFWWSY 44
DB 49 SGKLEFVQGNLERECMEKCSFEAREVFEVNTERTTEFWKQY 91

RESULT 12
US-09-884-901-3
/ Sequence 3, Application US/09884901
/ Patent No. US20020076798A1
/ GENERAL INFORMATION:
/ APPLICANT: Miao, Carol
/ APPLICANT: Kay, Mark
/ TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
/ FILE REFERENCE: UOPW-1-17396
/ CURRENT APPLICATION NUMBER: US/09/884,901
/ CURRENT FILING DATE: 2001-06-18
/ PRIOR APPLICATION NUMBER: US 60/212,902
/ PRIOR FILING DATE: 2000-06-20
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 3
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homosapien
US-09-884-901-3

Query Match          45.8%; Score 87; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRBSGLXRCXXKXLCSPXXAFKIFRNXXRTQFWWSY 44
DB 49 SGKLEFVQGNLERECMEKCSFEAREVFEVNTERTTEFWKQY 91

RESULT 13
US-09-759-130B-313
/ Sequence 313, Application US/09759130B
/ Publication No. US20030022279A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Frazer, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirtse, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wighton, Nicolas
/ APPLICANT: Goodheartl, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ FILE OF INVENTION: USFS.
/ FILE REFERENCE: MPI00-5350NMIM
/ CURRENT APPLICATION NUMBER: US/09/759,130B
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/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 313
/ LENGTH: 96
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          35.3%; Score 67; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 0.00018;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLXRCXXKXLCSPXXAFKIFRNXXRTQFWWSY 44
DB 46 GNLERECNEBLCYERAREIFVDEDKTIAFWQRY 79

RESULT 14
US-09-759-130B-312
/ Sequence 312, Application US/09759130B
/ Publication No. US20030022279A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Frazer, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirtse, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wighton, Nicolas
/ APPLICANT: Goodheartl, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ FILE OF INVENTION: USFS.
/ FILE REFERENCE: MPI00-5350NMIM
/ CURRENT APPLICATION NUMBER: US/09/759,130B
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
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/ ORGANISM: Homo sapiens
US-10-182-263-5

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 419;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRXCRXXLCSPXXAFXIFRNXXRTROFW 41
Db 1 ANSFLELRHSHSLERECIEICDFEAKKEIFQVDDTLAFW 41

RESULT 7
US-09-978-917A-4
/ Sequence 4, Application US/09978917A
/ Publication No. US20030027299A1
/ GENERAL INFORMATION:
/ APPLICANT: Maxygen Aps; Maxygen Holdings
/ TITLE OF INVENTION: Protein C or activated protein C-like molecules
/ FILE REFERENCE: 0219us310 - Protein C
/ CURRENT APPLICATION NUMBER: US/09/978,917A
/ CURRENT FILING DATE: 2001-10-17
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 419;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRXCRXXLCSPXXAFXIFRNXXRTROFW 41
Db 1 ANSFLELRHSHSLERECIEICDFEAKKEIFQVDDTLAFW 41

RESULT 8
US-10-182-263-2
/ Sequence 2, Application US/10182263
/ Publication No. US20030022354A1
/ GENERAL INFORMATION:
/ APPLICANT: Geriltz, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ CURRENT FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-182-263-2

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 461;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRXCRXXLCSPXXAFXIFRNXXRTROFW 41
Db 43 ANSFLELRHSHSLERECIEICDFEAKKEIFQVDDTLAFW 83

RESULT 9

/ ORGANISM: Homo sapiens
US-09-978-917A-2
/ Sequence 2, Application US/09978917A
/ Publication No. US20030027299A1
/ GENERAL INFORMATION:
/ APPLICANT: Maxygen Aps; Maxygen Holdings
/ TITLE OF INVENTION: Protein C or activated protein C-like molecules
/ FILE REFERENCE: 0219us310 - Protein C
/ CURRENT APPLICATION NUMBER: US/09/978,917A
/ CURRENT FILING DATE: 2001-10-17
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(42)
/ FEATURE:
/ NAME/KEY: CHAIN
/ LOCATION: (43)...(461)
US-09-978-917A-2

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 461;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRXCRXXLCSPXXAFXIFRNXXRTROFW 41
Db 43 ANSFLELRHSHSLERECIEICDFEAKKEIFQVDDTLAFW 83

RESULT 10
US-09-118-748-2
/ Sequence 2, Application US/09118748A
/ Patent No. US20020031799A1
/ GENERAL INFORMATION:
/ APPLICANT: Stafford, Darrel W.
/ APPLICANT: Chang, Jinli
/ TITLE OF INVENTION: Factor IX Antithemophilic Factor with Increased Clotting
/ TITLE OF INVENTION: Activity
/ FILE REFERENCE: 5470-183
/ CURRENT APPLICATION NUMBER: US/09/118,748A
/ CURRENT FILING DATE: 1998-07-17
/ EARLIER APPLICATION NUMBER: 60/053,571
/ EARLIER FILING DATE: 1997-07-21
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 415
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-118-748-2

Query Match
Best Local Similarity 45.8%; Score 87; DB 10; Length 415;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRGSLXRXCRXXLCSPXXAFXIFRNXXRTROFW 44
Db 3 SGKLEEFVQGNLERECMEKCSFEAREVVENTERTTEWKQY 45

RESULT 11
US-10-132-829-5
/ Sequence 5, Application US/10132829
/ Publication No. US20030044982A1
/ GENERAL INFORMATION:
/ APPLICANT: Chien, Kenneth R
/ APPLICANT: Hoshijima, Masahiko
/ TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
/ FILE REFERENCE: 6627-Pa1170
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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          47.9%; Score 91; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,1e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSILKRXCRXXLCSPFXAXFIIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSILKRXCRXXLCSPFXAXFIIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSILKRXCRXXLCSPFXAXFIIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSILKRXCRXXLCSPFXAXFIIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 / Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10GLU28PHE_4

Perfect score: 190
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Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	63.2	406	US-10-109-498-1	Sequence 1, Appl1
2	91	47.9	419	US-10-182-263-6	Sequence 6, Appl1
3	89	46.8	419	US-10-182-263-1	Sequence 3, Appl1
4	89	46.8	419	US-10-182-263-3	Sequence 4, Appl1
5	89	46.8	419	US-10-182-263-4	Sequence 5, Appl1
6	89	46.8	419	US-10-182-263-5	Sequence 2, Appl1
7	89	46.8	419	US-09-978-917A-4	Sequence 2, Appl1
8	89	46.8	461	US-10-182-263-2	Sequence 2, Appl1
9	89	46.8	461	US-09-978-917A-2	Sequence 2, Appl1
10	87	45.8	415	US-09-118-748-2	Sequence 2, Appl1
11	87	45.8	461	US-10-132-829-5	Sequence 5, Appl1
12	87	45.8	461	US-09-884-901-3	Sequence 3, Appl1
13	67	35.3	96	US-09-759-130B-312	Sequence 312, App
14	67	35.3	209	US-09-759-130B-312	Sequence 312, App
15	67	35.3	226	US-09-759-130B-310	Sequence 310, App
16	50	26.3	95	US-09-759-130B-356	Sequence 356, App
17	50	26.3	208	US-09-759-130B-355	Sequence 355, App
18	50	26.3	225	US-09-759-130B-353	Sequence 353, App
19	44	23.2	1438	US-10-006-091-1	Sequence 1, Appl1

20	44	23.2	1438	12	US-10-047-257-1	Sequence 1, Appl1
21	44	23.2	1471	12	US-10-095-718-2	Sequence 2, Appl1
22	44	23.2	2332	9	US-09-957-641-2	Sequence 2, Appl1
23	44	23.2	2351	9	US-10-132-829-4	Sequence 4, Appl1
24	42	22.1	233	10	US-09-867-550-1024	Sequence 1024, App
25	41	21.6	1431	12	US-10-095-718-4	Sequence 4, Appl1
26	40	21.1	1484	10	US-09-801-368-334	Sequence 334, App
27	39	20.5	197	9	US-10-076-622-516	Sequence 516, App
28	39	20.5	197	12	US-10-007-805-516	Sequence 516, App
29	39	20.5	232	9	US-10-076-622-517	Sequence 517, App
30	39	20.5	232	12	US-10-007-805-517	Sequence 517, App
31	39	20.5	243	9	US-09-938-418-7	Sequence 7, Appl1
32	39	20.5	243	9	US-10-045-992-4	Sequence 4, Appl1
33	39	20.5	243	9	US-10-063-547-122	Sequence 122, App
34	39	20.5	243	9	US-10-174-590-366	Sequence 366, App
35	39	20.5	243	9	US-10-176-758-366	Sequence 366, App
36	39	20.5	243	9	US-10-063-616-122	Sequence 122, App
37	39	20.5	243	9	US-10-175-737-366	Sequence 366, App
38	39	20.5	243	9	US-10-063-502-122	Sequence 122, App
39	39	20.5	243	9	US-10-076-622-514	Sequence 514, App
40	39	20.5	243	9	US-10-173-706-366	Sequence 366, App
41	39	20.5	243	9	US-10-175-738-366	Sequence 366, App
42	39	20.5	243	9	US-10-175-752-366	Sequence 366, App
43	39	20.5	243	9	US-10-176-482-366	Sequence 366, App
44	39	20.5	243	9	US-10-176-757-366	Sequence 366, App
45	39	20.5	243	9	US-10-176-913-366	Sequence 366, App

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      63.2%; Score 120; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1  ANGFLXLRREGSLRXCRXXLCSEFXAXAFXIFRNXXRTQFWVSY 44
Db      1  ANAFLLXLRREGSLRXCRXXKQCSFXAXRKFDAKXTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
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Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPXXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
 US-08-537-807-2
 ; Sequence 2, Application US/08537807
 ; Patent No. 5861374
 ; GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/537,807
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05779
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: US 08/065,725
 FILING DATE: 21-MAY-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,920
 FILING DATE: 28-FEB-1991
 ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 13952-8-1PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-467-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-537-807-2

Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPXXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
 US-08-871-003-2
 ; Sequence 2, Application US/08871003
 ; Patent No. 5997864
 ; GENERAL INFORMATION:

APPLICANT: Hart, Charles E.
 APPLICANT: Petersen, Lars C.
 APPLICANT: Hedner, Ulla
 APPLICANT: Rasmussen, Mirella E.
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Zymogenetics, Inc.
 STREET: 1201 Baslake Avenue East
 CITY: Seattle

STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/871,003
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Sawisjak, Deborah A
 REGISTRATION NUMBER: 37,438
 REFERENCE/DOCKET NUMBER: 90-0707
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-871-003-2

Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPXXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:20
 Job time: 10.75 secs

FILING DATE: 21-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match 63.2%; Score 120; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 3.5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCRXKXLCSPFXAFIFRNXXRTROFWVY 44
DB 39 ANAFLELRPGSLERCKEQCSFEARERIFKDAERTKLFWISY 82

RESULT 12
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 63.2%; Score 120; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 3.5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCRXKXLCSPFXAFIFRNXXRTROFWVY 44
DB 39 ANAFLELRPGSLERCKEQCSFEARERIFKDAERTKLFWISY 82

RESULT 13
US-08-660-289-2
Sequence 2, Application US/08660289

Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: T8R1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 63.2%; Score 120; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAFIFRNXXRTROPWVSY 44
DB 1 ANAFLELRPGSLRERCKEQCSFEERAREIFKDAERTKLFWISY 44

RESULT 10
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC80472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 63.2%; Score 120; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAFIFRNXXRTROPWVSY 44
DB 1 ANAFLELRPGSLRERCKEQCSFEERAREIFKDAERTKLFWISY 44

RESULT 11
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/065,725

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; GENERAL INFORMATION:
; APPLICANT: Nicolaesen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agrib, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129,224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-293-778-24

Query Match 63.2%; Score 120; DB 1; Length 406;
Best Local Similarity 52.3%; Pred.No.3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLLREGSLXRCRXLLCSFXXAFIFRNXXRTROPFWSY 44
Db 1 ANAFLLYLRLPGSLRYCKYQCSFYARIFYKDAYTKLFWISY 44

RESULT 8
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Filling, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSKI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match 63.2%; Score 120; DB 1; Length 406;
Best Local Similarity 52.3%; Pred.No.3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLLREGSLXRCRXLLCSFXXAFIFRNXXRTROPFWSY 44
Db 1 ANAFLEELRPGSLRLRCKEKGCSFEAREIFKDAYTKLFWISY 44

RESULT 9
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
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; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28
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Query Match          67.9%; Score 129; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 8.2e-16;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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Oy      1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXRTROPFVSY 44
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Db      1 ANAFLXXLRGSLRXCRXXLCSPFXAXFIKDXARTKLFWISY 44
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RESULT 3
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
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Query Match          66.3%; Score 126; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 2.8e-15;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy      1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXRTROPFVSY 44
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 ANAFLXXLRGSLRXCRXXLCSPFXAXFIKDXARTKLFWISY 44
```

```
RESULT 4
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match          64.7%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 9.3e-15;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy      1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXRTROPFVSY 44
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 ANAFLXXLRGSLRXCRXXLCSPFXAXFIKDXARTKLFWISY 44
```

```
RESULT 5
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match          63.7%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2.1e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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```
Oy      1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXRTROPFVSY 44
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 ANAFLXXLRGSLRXCRXXLCSPFXAXFIKDXARTKLFWISY 44
```

```
RESULT 6
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
```

```
Query Match          63.2%; Score 120; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.1e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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```
Oy      1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXRTROPFVSY 44
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 ANAFLXXLRGSLRXCRXXLCSPFXAXFIKDXARTKLFWISY 44
```

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RESULT 7
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
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Thu Mar 20 14:52:19 2003

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Page 8

Search completed: March 19, 2003, 15:13:40
Job time : 46.3125 secs

```
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match          45.8%; Score 87; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
```

RESULT 14

```
O9PTW7 PRELIMINARY; PRT; 608 AA.
ID O9PTW7;
AC O9PTW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prothrombin.
GN OSPT.
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_TaxID=8801;
RN [1]
RP TISSUE=LIVER;
RC MEDLINE=20579470; PubMed=1137455;
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
RT "Purification and characterization of ostrich prothrombin.";
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; AB028871; BA89046.1; -.
DR HSSP; P00734; 1UVS.
DR MEROPS; S01.217; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000001; Kringleg.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00051; kringleg; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; kringleg; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
```

SQ SEQUENCE 608 AA; 69392 MW; 11B974B9A5E54EA2 CRC64;

Query Match 45.8%; Score 87; DB 13; Length 608;

Best Local Similarity 35.7%; Pred. No. 1.3e-07;

Matches 15; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

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OY 3 GFLXLRREGSLKRCXKXLLCSFXXAFIIRNXXRTROFWVSY 44
DB 47 GFLXLRREGSLKRCXKXLLCSFXXAFIIRNXXRTROFWVSKY 88
```

RESULT 15

```
O9GMD9 PRELIMINARY; PRT; 469 AA.
ID O9GMD9;
AC O9GMD9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=1132153;
RA Poorafshar M., Aveskog M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
RT monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; AF275654; AAG0453.1; -.
DR HSSP; P00742; 1XKB.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match          45.3%; Score 86; DB 6; Length 469;
Best Local Similarity 34.1%; Pred. No. 1.6e-07;
Matches 15; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
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OY 1 ANGFLXLRREGSLKRCXKXLLCSFXXAFIIRNXXRTROFWVSY 44
DB 41 ANGFLXLRREGSLKRCXKXLLCSFXXAFIIRNXXRTROFWVSKY 84
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88377116; PubMed=3416069;
RA Reiteme P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Brier E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033463; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0010; EGFBLOOD.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TRYSPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 45.8%; Score 87; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRREGSLRXCRXXLCSPXAFIRNXXRTQRFVWSY 44
Db 44 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 86

RESULT 12
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor XI.
F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 45.8%; Score 87; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRREGSLRXCRXXLCSPXAFIRNXXRTQRFVWSY 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 13
Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor XI.
F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.

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DR PROSITE; PS01187; EGF_CA.1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXXLCSEFXAFLFRNXXTRQFWVS 44
Db 41 ANSFEEFKKGNLERECMEICSEYEVREIFEDDEKTKEWTKY 84

RESULT 9
088947 ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X."
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129S1;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene."
RL Thromb. Haemost. 0:0-0(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

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DR PROSITE; PS01187; EGF_CA.1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MW; 8AC09DE5F9D271E CRC64;

Query Match
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXXLCSEFXAFLFRNXXTRQFWVS 44
Db 41 ANSFEEFKKGNLERECMEICSEYEVREIFEDDEKTKEWTKY 84

RESULT 10
015253 ID 015253 PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PFI.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; GLA_1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KM Signal.
FT SIGNAL 1 43
FT CHAIN 44 >100
FT NON TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FDB5D0174E1F6FE CRC64;

Query Match
Best Local Similarity 38.6%; Pred. No. 2.3e-08;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXXLCSEFXAFLFRNXXTRQFWVS 44
Db 44 ANTFLEVRKGNLERECVETCSYBEAFALSSSTATDVFWAKY 87

RESULT 11
014316 ID 014316 PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).

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DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PR00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00889; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KM Hydroxylation; Repeat; Serine protease
 SQ SEQUENCE 482 AA; 54265 MW; 02846783954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
 Best Local Similarity 36.4%; Pred. No. 8e-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRCRXKLCSPFXAFLFRNXXRTROFWVS 44
 DB 41 ANSFEEIKKGNLERECVEECISFEAREVFEDEKTEFWNKY 84

RESULT 7
 OS4740 PRELIMINARY; PRT; 481 AA.
 ID OS4740;
 AC OS4740;
 DT 01-JUN-1998 (Tremblrel_06, Created)
 DT 01-JUN-1998 (Tremblrel_06, Last sequence update)
 DT 01-JUN-2002 (Tremblrel_21, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6).
 GN F10 OR FA10.
 OS Mus musculus (Mouse).
 OC Plasmid DBLuescript.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=8454993; PubMed=9783672;
 RA Heidemann H.H., Kontermann R.B.;
 RT Cloning and recombinant expression of mouse coagulation factor X.";
 RL Thromb. Res. 92:33-41(1998).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AJ222677; CAAL0933.1; -
 DR HSSP: P00742; IYKA.
 DR MEROPS: S01.216; -.
 DR MGD: MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF_like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00889; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
 KM Repeat; Serine protease; Signal.
 FT SIGNAL 1 40
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 2.9e-08;
 Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRCRXKLCSPFXAFLFRNXXRTROFWVS 44
 DB 41 ANSFEEIKKGNLERECVEECISYEVRLEIFEDDKTEYWTY 84

RESULT 8

Q99LJ2 PRELIMINARY; PRT; 481 AA.

ID Q99LJ2;
 AC Q99LJ2;
 DT 01-JUN-2001 (Tremblrel_17, Created)
 DT 01-JUN-2001 (Tremblrel_17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel_21, Last annotation update)
 DE Coagulation factor X.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: BC003877; AA03877.1; -
 DR HSSP: P00742; IYKA.
 DR MEROPS: S01.216; -.
 DR MGD: MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF_like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_I1.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00889; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.

```
RT "Complete sequence of UC72A01."
CC Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; AF318182; AK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 51.6%; Score 98; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 8.9e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLLCSFYXAFXIFRNXXRTQGFVSY 44
Db 42 ANSFLEBRPGLRRCMEICDLEEAQEIFQVNDTLAWMYKY 85

RESULT 5
Q9TR0 PRELIMINARY; PRT; 456 AA.
AC Q9TR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
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DR EMBL; AJ001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59F CRC64;

Query Match 50.5%; Score 96; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 2.1e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLLCSFYXAFXIFRNXXRTQGFVSY 44
Db 43 ANSFLEBRPGLRRCMEICDFFEEAKEIFQVNDTLAWMYKY 86

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 63.2%; Score 120; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 1e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSIXKCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 61 ANAPLEELRPGSLERECNEBQCSFEAREIFKDAERTKLFWIST 104

RESULT 2
Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E8FCC274 CRC64;

Query Match 54.7%; Score 104; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 6.7e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSIXKCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 42 ANSFLERMPGSLERECNEBQCSFEAREIFQNVEDTLAFWIKY 85

RESULT 3
Q61109 PRELIMINARY; PRT; 446 AA.
AC Q61109;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U44795; AAC82570.1; -.
DR HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002066; Aldehyde dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KM Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEPDA6870 CRC64;

Query Match 54.2%; Score 103; DB 11; Length 446;
Best Local Similarity 47.7%; Pred. No. 1e-10;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBGSIXKCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 42 ANSLLEELMPGSLERECNEBQCSFEAREIFKSPERTKQFWIVY 85

RESULT 4
Q99PC6 PRELIMINARY; PRT; 460 AA.
AC Q99PC6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
```

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10glu28phe_4
Perfect score: 190
Sequence: 1 ANGFLXXLRSGSLKRXCRXX.....XXAFXIFNNXXRTQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	63.2	701	4 Q96PQ8	Q96PQ8 homo sapien
2	104	54.7	460	11 Q91MN8	Q91MN8 mus musculu
3	103	54.2	446	11 Q61109	Q61109 mus musculu
4	98	51.6	460	11 Q99PC6	Q99PC6 mus musculu
5	96	50.5	456	6 Q91TPO	Q91TPO canis fam1
6	93	48.9	482	11 Q63207	Q63207 rattus norv
7	90	47.4	481	11 Q54740	Q54740 mus musculu
8	90	47.4	481	11 Q99L32	Q99L32 mus musculu
9	90	47.4	481	11 Q88947	Q88947 mus musculu
10	87	45.8	456	4 Q15253	Q15253 homo sapien
11	87	45.8	456	4 Q14316	Q14316 homo sapien
12	87	45.8	461	6 Q95ND7	Q95ND7 pan troglod
13	87	45.8	461	6 Q95ND6	Q95ND6 pan troglod
14	87	45.8	608	13 Q9PTW7	Q9PTW7 struthio ca
15	86	45.3	469	6 Q95MD9	Q95MD9 ornithorhyn
16	85	44.7	49	6 Q95ME8	Q95ME8 bos taurus

17	78	41.1	138	6 Q28994	Q28994 sus scrofa
18	77	40.5	433	13 Q90YK1	Q90YK1 brachydanio
19	75	39.5	607	13 Q91001	Q91001 gallus gall
20	74	38.9	648	6 Q29094	Q29094 sus scrofa
21	73	38.4	399	11 Q9COW3	Q9COW3 mus musculu
22	70.5	37.1	542	5 Q8TF13	Q8TF13 halocynthia
23	69	36.3	650	4 Q9NSD0	Q9NSD0 homo sapien
24	69	36.3	650	4 Q16519	Q16519 homo sapien
25	68	35.8	179	4 Q8TAS3	Q8TAS3 homo sapien
26	68	35.8	198	11 Q8R182	Q8R182 mus musculu
27	58	30.5	25	11 Q9QVH6	Q9QVH6 rattus norv
28	58	30.5	678	4 Q14393	Q14393 homo sapien
29	57	30.0	673	11 Q61592	Q61592 mus musculu
30	57	30.0	674	11 Q99K57	Q99K57 mus musculu
31	55	28.9	674	11 Q63772	Q63772 rattus norv
32	54	28.4	98	13 P82807	P82807 notechis sc
33	51	26.8	130	12 Q9DUB8	Q9DUB8 tt virus
34	50	26.3	184	10 Q91VFL	Q91VFL arabidopsis
35	47.5	25.0	575	10 Q94E17	Q94E17 oryza sativ
36	47.5	25.0	608	10 Q9XF36	Q9XF36 medicago sa
37	46.5	24.5	196	10 Q04284	Q04284 selaginella
38	46.5	24.5	567	10 Q8W4J2	Q8W4J2 arabidopsis
39	46.5	24.5	603	10 Q91PG7	Q91PG7 arabidopsis
40	46.5	24.5	606	10 Q9S1G9	Q9S1G9 arabidopsis
41	46.5	24.5	651	10 Q8S218	Q8S218 oryza sativ
42	46	24.2	174	2 Q93FY1	Q93FY1 bruceella ab
43	45.5	23.9	249	5 Q9YVS0	Q9YVS0 drosophila
44	45.5	23.9	431	10 Q94EY5	Q94EY5 arabidopsis
45	45.5	23.9	492	10 Q9SMU7	Q9SMU7 cicler arlet

ALIGNMENTS

RESULT 1

Q96PQ8 PRELIMINARY, PRT, 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocognate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAKS686.1; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GIA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; GIA_1.
DR Pfam: PF00047; Ig_2.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00181; EGF_2.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.

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RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE=9238094; PubMed=1517205;
RA Nishimura H., Takeo T., Hase S., Shimoniishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue";
RL J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX";
RL (in) Abstracts of Xth International conference on methods in protein
RL structure analysis, pp.50-50, Annecy (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=20575397; PubMed=1133752;
RA Aruda V.R., Hagerstrom J.N., Delich J., Helman-Patterson T.,
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RA Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX";
RL Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=95229607; PubMed=7733897;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy";
RL J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96032604; PubMed=7547952;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX";
RL Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96279169; PubMed=8663165;
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RA Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX";
RL J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=97199336; PubMed=9047312;
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hisey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm";
RL Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE=91308127; PubMed=1854745;
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX";
RL Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE=93284090; PubMed=1304885;
RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha";
RL Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
RX MEDLINE=95330802; PubMed=7606779;

RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
RT "The structure of a Ca(2+)-binding epidermal growth factor-like
RT domain: its role in protein-protein interactions";
RL Cell 82:131-141(1995).
RN [26]
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 45.8%; Score 87; DB 1; Length 461;
Best Local Similarity 39.5%; Pred. No. 5, 4e-08;
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QY 2 NGFLXXLRGGSLXRXCRXXLCSPFXAPXIFRNXXRTTROPFVSY 44
DB 49 SGKLEEFVQGNLERBCEMEKCSFEAREVFPENTRTTFWKQY 91

Search completed: March 19, 2003, 14:52:58
Job time : 6.625 secs

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT_SITE 275 275 CHARGE RELAY SYSTEM.
FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT_SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 46.8%; Score 89; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 2.5e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLXRCRXXLCSPFXAFLFRNXXRTQRFVSY 44
Db 41 ANSFLEEVKQGNLRECELEACSLSEAREVEDAQTDEFWSKY 84

RESULT 15
FA9_HUMAN STANDARD; PRT; 461 AA.
ID P00740;
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX 1;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
factor B).";
RL Biochemistry 24:3736-3750(1985).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham J.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
RN 3;
RP SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Gianneli F., Gould K.G.,
RA Huddleston J.A., Brownlee G.G.;
RT "The gene structure of human anti-haemophilic factor IX.";
RL EMBO J. 3:1053-1060(1984).
RN 4;
RP SEQUENCE FROM N.A.
RX MEDLINE=83220788; PubMed=6687940;
RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohli V.,
RA Finkelstein A., Tolstoshev P., Lecocq J.P.;
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
unique 52-base synthetic oligonucleotide probe deduced from the amino
acid sequence of bovine factor IX.";
RL Nucleic Acids Res. 11:2325-2335(1983).
RN 5;
RP SEQUENCE OF 36-326 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=84300526; PubMed=6089357;
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
RT "Isolation and characterization of human factor IX cDNA."

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RT identification of Tag I polymorphism and regional assignment.";
RL Somatic. Cell Mol. Genet. 10:465-473(1984).
RN 6;
RP SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE=88127096; PubMed=3340835;
RA Stoflet E.S., Koebert D.D., Sarkar G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing.";
RL Science 239:491-494(1988).
RN 7;
RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE=94054330; PubMed=8236150;
RA de la Salle C., Charmanier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN 8;
RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
RX MEDLINE=90078229; PubMed=2592373;
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
tryptophan and its activation by alpha-chymotrypsin and rat mast cell
chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN 9;
RP HYDROXYLATION OF ASP-110.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN 10;
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=78194509; PubMed=659613;
RA di Scipio R.G., Kurachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN 11;
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185715; PubMed=6425296;
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
RL J. Biol. Chem. 259:5698-5704(1984).
RN 12;
RP ERRATUM.
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2583-2583(1985).
RN 13;
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=86189947; PubMed=3009023;
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
by mutation of arginine to glutamine at position -4.";
RL Cell 45:343-348(1986).
RN 14;
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
(Xyl2-Glc) O-glycosidically linked to a serine residue in the first
epidermal growth factor-like domain of human factors VII and IX and
protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN 15;
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).

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RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein Cvermont: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Mura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tenngborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandrille S., Vdaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gonaud-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
 RA Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gandrille S., Alhenc-Gelas M., Gausem P., Allaud M.-F., Dupuy E.,
 RA Uhan-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-166(1993).
 RN [21]
 RP VARIANTS G-14; Q-21; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Fabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous

RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomey R.R., McPherson R.A., Fucci J.C.,
 RA Koerber M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patraccini P., Gemmati D., Caetaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
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 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
 Oy 1 ANGFLXLYREGSLXRCXRLCSFXAFXIFRNXXRTROFW 41
 Db 43 ANSFLELRHSSLERECIEICDFEEAKEIFQWVDTLAFW 83
 RESULT 14
 ID FA10 BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Pung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130561; PubMed=6766735;
 RA Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Tilani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kistel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Tilani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";

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FT DOMAIN 125 165 EGF-LIKE 2.
FT MOD_RES 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 /FTID=CAR_000013.
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FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

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Query Match 48.9%; Score 93; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 4,7e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRGSLRXCRXXLCSPXXAFXIFRXXRTQRFWXY 44
Db 41 ANGFLEEMKXGHLERECMEETCSYEAREVFEDSDKNTNEWMXK 84

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RESULT 13
PRIC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K-dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Sautter R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).

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RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RL "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J., Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Machner T., Oganesyan V., Hof F., Huber R., Foundling S., Eamon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Glu-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitema P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitollie A., Talbot S., Bevan D., Kakkay V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitema P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";

```

RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGallivray R.T.A.;
 RT "characterization of an almost full-length cDNA coding for human
 blood coagulation factor X";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 cDNA";
 RL Gene 41:311-314(1986).
 [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
 Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 coagulation factor X: evidence for identification of residue 63 as
 beta-hydroxyaspartic acid";
 RL Biochemistry 22:2875-2884(1983).
 [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 peptides of blood coagulation factor X. The role of the carbohydrate
 moieties in the activation of factor X";
 RL Eur. J. Biochem. 218:153-163(1993).
 [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusnam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 encoding human factor X";
 RL Gene 84:517-519(1989).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution";
 RL J. Mol. Biol. 232:947-966(1993).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 factor Xa";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 [11]
 RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 converts prothrombin to thrombin in the presence of factor Va,
 calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: K03194; AAA52490.1; --
 DR EMBL: M57285; AAA52421.1; --
 DR EMBL: L29433; AAA52764.1; --
 DR EMBL: L00390; AAA52764.1; JOINED.
 DR EMBL: L00391; AAA52764.1; JOINED.
 DR EMBL: L00392; AAA52764.1; JOINED.
 DR EMBL: L00393; AAA52764.1; JOINED.
 DR EMBL: L00394; AAA52764.1; JOINED.
 DR EMBL: L00395; AAA52764.1; JOINED.
 DR EMBL: L00396; AAA52764.1; JOINED.
 DR EMBL: M22613; AAA51984.1; --
 DR EMBL: K01886; AAA52486.1; --
 DR EMBL: M31297; AAA52636.1; --
 DR PIR: A00924; EXHU.
 DR PIR: A25853; A25853.
 DR PIR: A24478; A24478.
 DR PDB: 1HCG; 08-MAY-95.
 DR PDB: 1FXI; 29-OCT-97.
 DR PDB: 1FXI; 17-JUN-98.
 DR PDB: 1XXA; 23-MAR-99.
 DR PDB: 1XXB; 23-MAR-99.
 DR MEROPS: S01.216; --
 DR GlycoStatedB: P00742; --
 DR Genew: HGNC:3528; P10.
 DR MIM: 134530; --
 DR MIM: 227600; --
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PR00089; EGF_2.
 DR Pfam: PR00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYD_Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein: Hydroxylase; Serine protease; Plasma; Blood coagulation;
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31
 FT PROPEP 32 40
 FT CHAIN 41 179 FACTOR X LIGHT CHAIN.
 FT CHAIN 183 488 FACTOR X HEAVY CHAIN.
 FT PROPEP 183 234 ACTIVATION PEPTIDE.
 FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Eason N.L., Lane T.M., Eason C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid."
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-----
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CC EMBL: K02435; AAA30685.1; -.
CC DR PIR: A00928; KXBO.
CC DR HSP: P04070; LPCU.
CC DR MEROPS: S01.218; -.
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR001881; EGF Ca.
CC DR InterPro: IPR001254; Ser_protease_Try.
CC DR InterPro: IPR000294; VitK_dep_GLA.
CC DR Pfam: PF00008; EGF_2.
CC DR Pfam: PF00089; trypsin; 1.
CC DR Pfam: PF00594; gla; 1.
CC DR SMART: SM00181; EGF; 2.
CC DR SMART: SM00069; GLA; 1.
CC DR SMART: SM00020; TRYD_SPC; 1.
CC DR PROSITE: PS00010; ASX_HYDROXYL; 1.
CC DR PROSITE: PS00022; EGF_1; 1.
CC DR PROSITE: PS01186; EGF_2; 2.
CC DR PROSITE: PS01187; EGF_CA; 1.
CC DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC DR PROSITE: PS00014; TRYPSIN_DOM; 1.
CC DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
CC NON_TER 1
FT SIGNAL 1
FT PROPEP 29
FT CHAIN 30 39
FT CHAIN 40 194
FT PEPTIDE 197 456
FT DOMAIN 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456

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FT MOD_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 110 110 HYDROXYLATION.
FT ACT_SITE 252 252 CHARGE RELAY SYSTEM.
FT ACT_SITE 298 298 CHARGE RELAY SYSTEM.
FT ACT_SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 227 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .).
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAAFE633F94C209 CRC64;

Query Match 49.5%; Score 94; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 2.9e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGLFXXLRGSLRXCRXLCSPFXAFPIFRNXXTRQFWYSY 44
DB 40 ANSFLERLRPGNVERECSEVCEFEERARLFOVTEDTMAFWSEY 83

RESULT 12
FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.V., Pittman D.D., Long G.L., Kaufman R.U., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X."
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RL protein C."
RN Biochemistry 25:5098-5102(1986).
RN [3]

```


CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC chrombin-chromomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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 CC EMBL; AF191307; AAC28380.1; -.
 DR HSSP; P04070; 1PCU.
 DR MEROPS; S01.218; -.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000284; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00001; EGF-like; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 DR Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 DR EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 DR SIGNAL; 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67

FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 52.1%; Score 99; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 3.7e-10;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGEFLXXREGSLRXCRXXLCSFXXAFIPRXRXTRQFWWSY 44
 DB 42 ANSFLERLPSSLERCKEKTCDFEAREIFONTENTMAFWSKY 85
 RESULT 10
 FA10 RABIT STANDARD; PRT; 490 AA.
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R.; Anderson K.D.; James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X.";
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 112 112 GAMMA-CARBOXYGLUTAMIC ACID
FT ACT_SITE 254 254 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT DISULFID 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664BDACD5 CRC64;

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Query Match Best Local Similarity 45.2%; Score 103; DB 1; Length 461;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXKRCXKXLCFXXAFIRNXXRTQFVWSY 44
42 ANSFLFVRAGLTERECMEICDFEAEQIFQWEDTLAFWIKY 85

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RESULT 8
ID TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9B2D7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylglutamic acid protein 3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=2117044; PubMed=1171957;
RA Kolman J.D., Harris J.E., Xie L., Davie E.W.;
RT Identification of two novel transmembrane gamma-carboxylglutamic acid
RT proteins expressed broadly in fetal and adult tissues.
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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or send an email to license@sib-sib.ch).

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CC EMBL; AF326350; AAK00955.1; -.
CC HSSP; P00740; 1CFH.
CC InterPro; IPR002383; GLA blood.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00069; GLA; 1.
CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
CC Gamma-carboxylglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 78 PROTEIN 3.
FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 102 231 POTENTIAL.
FT DOMAIN 23 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; 8A373EA48490D81 CRC64;

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Query Match Best Local Similarity 52.6%; Score 100; DB 1; Length 231;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXKRCXKXLCFXXAFIRNXXRTQFVWSY 44
20 ANSFLFVRAGLTERECMEICSYEYKEVFNKKETMFWKGY 63

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RESULT 9
ID PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin K dependent protein C precursor (BC 3.4.21.69)
DE (Anticprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=2112490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neane P.J.,
RA Kim H.K.W.;
RT Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains.
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.

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KW EGF-like domain; Repeat; signal: Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 169
FT DOMAIN 134 446
FT SITE 193 194
FT ACT SITE 224 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 225
FT DISULFID 351 370
FT DISULFID 381 409
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT CARBOHYD 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA; 50276 MW; 2512E44A5C96E CRC64;

Query Match 54.2%; Score 103; DB 1; Length 446;
Best Local Similarity 47.7%; Pred. No. 6, 7e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLEEGSLRXCRXXLCSFXXAFYFRXXRTROFWVSY 44
Db 42 ANSLLEELMPGSLERECNEBOCSFFERARELFKSPERTKQFWIVY 85

RESULT 7
PRTC RAT ID PRTC RAT STANDARD; PRT; 461 AA.
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).

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CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL, X64316; CAA4567.1; -.
CC PIR, S18994; S18994.
CC PIR, S24312; S24312.
CC HSP, P04070; 1PCU.
CC DR MEROPS, S01.218; -.
CC DR InterPro: IPR000152; Asx hydroxyl.
CC DR InterPro: IPR000314; Chymotrypsin.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR001381; EGF Ca.
CC DR InterPro: IPR002383; GLA blood.
CC DR InterPro: IPR001254; Ser protease Try.
CC DR InterPro: IPR000294; VitK_dep_GLA.
CC DR Pfam, PF00008; EGF, 2.
CC DR Pfam, PF00089; tryptsin, 1.
CC DR Pfam, PF00594; gla, 1.
CC DR PRINTS, PR00722; CHYMOTRYPSIN.
CC DR PRINTS, PR00001; GLABLOOD.
CC DR SMART, SM00179; EGF_CA, 1.
CC DR SMART, SM00061; EGF_Like, 1.
CC DR SMART, SM00069; GLA, 1.
CC DR SMART, SM00020; TRY_SPC, 1.
CC DR PROSITE, PS00010; ASX_HYDROXYL, 1.
CC DR PROSITE, PS00022; EGF_1, 1.
CC DR PROSITE, PS01186; EGF_2, 2.
CC DR PROSITE, PS01187; EGF_CA, 1.
CC DR PROSITE, PS00011; GLU_CARBOXYLATION, 1.
CC DR PROSITE, PS50240; TRYPSIN_DOM, 1.
CC DR PROSITE, PS00134; TRYPSIN_HIS, 1.
CC DR PROSITE, PS00135; TRYPSIN_SER, 1.
CC KW Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hyaluronase; Signal.
CC KW EGF-like domain; Repeat; signal: Hydroxylation.
FT SIGNAL 1 32
FT PROPEP 33 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 48 48
FT MOD_RES 48 48

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00135; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
FT SEQUENCE 461 AA; 51945 MW; 53FA0D85B194D5E CRC64;

Query Match 54.7%; Score 104; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 4.6e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

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1 ANGFLXXLRGSLKRXCRXXLCSEFXAXIFRNXXRTQFWVSY 44
42 ANSFLBEMRPGSLERECMBEICDFEBAQIFQWVEDTLAFWIKY 85

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RESULT 6
ID FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
OS F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127157; PubMed=8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene.
RL Thromb. Haemostas. 76:957-964(1996).
CC -|- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VIIA IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -|- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -|- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -|- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; U66079; AAC3796.1; -.
DR HSSP; P08709; 1BF9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00023; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RT Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; ICFH.
DR Genew; HNC:9469; PRRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83
FT TRANSMEM 84 106
FT DOMAIN 107 218
FT DOMAIN 24 61
FT DOMAIN 131 135
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 56.3%; Score 107; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 6.3e-12;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRYCRXXLCSFYXAFXIFRNXXRTQFQWVSY 44
Db 21 ANGFEIRGNGNIERECKEFTFEARFAFENNEKTFEWFSTY 64

RESULT 5
PRIC MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RX Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
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RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RX MEDLINE=98152576; PubMed=9493582;
RX Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RX Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RX Murakawa M., Okamura T., Kamura T., Kuroiwa M., Hara M., Nino Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; DA3755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
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DR PRINTS; PR00722; CHYNOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPE 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 203
FT DISULFID 198 233
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SO SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 67.4%; Score 128; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2; Ie-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
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RESULT 3
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie B.W.;
RT "Characterization of a cDNA coding for human factor VII."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaesen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells."
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foester D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine."
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimoniishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z."
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=9144709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first BGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Kontigsberg W.H., Newreson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor."
RL Nature 380:41-46(1996).
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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT ACT_SITE 242 242 FACTOR VII HEAVY CHAIN.
FT ACT_SITE 344 344 GLA-RICH.
FT BINDING 338 338 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 17 22 EGF-LIKE 2.
FT DISULFID 50 61 SERINE PROTEASE.
FT DISULFID 55 70 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
FT DISULFID 72 81 FACTOR IXA, OR THROMBIN).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 O-LINKED (GLC. . .).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
FT CARBOHYD 407 AA; 44431 MM; 703E1FE0636F7F10 CRC64;
SQ SEQUENCE

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Query Match Similarity 77.9%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 4.6e-19;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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OY 1 ANGFLXXLRGSLXRCYKXLLCSFXAXAFYIPNXXXTROFWWSY 44
Db 1 ANGFLEELLPGSLERCRELTCSFEAAHFIIFNEERTROFWWSY 44

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=liver;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL Blajchman M.A., Clarke B.J., Sheffield W.P., Brothers A.B.,
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -.
DR HSPF; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds

(without alignments)
328.082 Million cell updates/sec

Title: 10g1u28phe_4

Perfect score: 190
Sequence: 1 ANGFLXLRREGSLKRXCRXX.....XXAFXI FRNXKTRQFWWSY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	77.9	407	1	FA7_BOVIN
2	128	67.4	444	1	FA7_RABIT
3	120	63.2	466	1	FA7_HUMAN
4	107	56.3	218	1	TMG1_HUMAN
5	104	54.7	461	1	PRTC_MOUSE
6	103	54.2	446	1	FA7_MOUSE
7	103	54.2	461	1	PRTC_RAT
8	100	52.6	231	1	TMG3_HUMAN
9	99	52.1	459	1	PRTC_PIG
10	97	51.1	490	1	FA10_RABIT
11	94	49.5	456	1	PRTC_BOVIN
12	93	48.9	488	1	FA10_HUMAN
13	89	46.8	461	1	PRTC_HUMAN
14	89	46.8	492	1	FA10_BOVIN
15	87	45.8	461	1	FA9_HUMAN
16	87	45.8	622	1	THRB_HUMAN
17	85	44.7	416	1	FA9_BOVIN
18	84	44.2	617	1	THRB_RAT
19	84	44.2	618	1	THRB_MOUSE
20	82	43.2	458	1	PRTC_RABIT
21	81	42.6	475	1	FA10_CHICK
22	80	42.1	452	1	FA9_CANFA
23	80	42.1	459	1	FA9_MOUSE
24	78	41.1	625	1	THRB_BOVIN
25	69	36.3	400	1	PRTC_HUMAN
26	69	36.3	649	1	PRTC_HUMAN
27	69	36.3	675	1	PRTC_MACMU
28	69	36.3	676	1	PRTC_BOVIN
29	68	35.8	202	1	TMG2_HUMAN
30	68	35.8	646	1	PRTC_HUMAN
31	67	35.3	226	1	TMG4_HUMAN
32	66	34.7	376	1	FA10_TROCA
33	66	34.7	675	1	PRTC_RAT

34	65	34.2	396	1	PRTC_BOVIN	P00744 bos taurus
35	59	31.1	675	1	PRTC_MOUSE	Q08761 mus musculus
36	52	27.4	604	1	VE1_BPv2	P11298 bovine papl
37	52	27.4	605	1	VE1_BPv1	P03116 bovine papl
38	48.5	25.5	2133	1	FA8_PIG	P12263 sus scrofa
39	48	25.3	413	1	NCAP_IHNV	P19691 infectio
40	44	23.2	2351	1	FA8_HUMAN	P00451 homo sapien
41	42.5	22.4	105	1	UL03_HCMVA	P16775 human cytom
42	42	22.1	320	1	GSHB_BUCAI	P57612 buchneera ap
43	41	21.6	97	1	YCRB_MYCCA	P45619 mycoplasma
44	41	21.6	315	1	YDJH_ECOLI	P77493 escherichia
45	41	21.6	348	1	EXOO_RHIME	P33697 rhizobium m

ALIGNMENTS

RESULT 1	FA7_BOVIN	STANDARD;	PRT;	407 AA.
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AC	P22457;			
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DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-UTN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89008362; PubMed=3049594;			
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,			
RA	Iwanaga S.;			
RT	"Bovine factor VII. Its purification and complete amino acid			
RT	sequence.";			
RL	J. Biol. Chem. 263:14868-14877(1988).			
RN	[2]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=2129367;			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RT	"A new triasaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RL	Adv. Exp. Med. Biol. 281:121-131(1990).			
CC	- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS			
CC	CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIIa, FACTOR IXa, OR			
CC	THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR			
CC	AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa			
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO			
CC	FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.			
CC	- CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-Ile bond in factor X to			
CC	form factor Xa.			
CC	- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED			
CC	BY A DISULFIDE BOND.			
CC	- TISSUE SPECIFICITY: PLASMA.			
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.			
DR	PIR; A31979; A31979.			
DR	HSSP; P08709; 1BF9.			

Thu Mar 20 14:52:17 2003

10g1u28phe_4.rpr

Page 10

Search completed: March 19, 2003, 15:01:00
Job time : 30.125 secs

1
.
2

A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-26/Domain: signal sequence #status experimental <PPT>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <Gla>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EG2>
 F:134-170/Domain: EGF homology <EG2>
 F:227-266/Domain: activation peptide #status experimental <ACT>
 F:227-261/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:237-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F:99/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
 F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 45.8%; Score 87; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1.8e-07;
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXLRBGSGLKRCXKXLCSPFXAFIFRNKXRTQFWVS 44
 Db 49 SGLKEFVQGNLERECMEKCSFEAREVFENTERTTFWQY 91

RESULT 12

Thrombin (EC 3.4.21.5) precursor [validated] - human
 N:Alternate names: coagulation factor II

N:Contents: prothrombin

C:Species: Homo sapiens (man)

C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000

C:Accession: A29351; A00914; B00914; A37549; A37550; I51952

R:Degem, S.J.F.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A:Title: Nucleotide sequence of the gene for human prothrombin.

A:Reference number: A29351; MUID:88077877; PMID:12825773

A:Accession: A29351

A:Molecule type: DNA

A:Residues: 1-622 <DEG>

A:Cross-references: GB:M17262; GB:M33691; NID:G558069; PIDN:AAC63054.1; PID:G339641

R:Degem, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.

Biochemistry 22, 2087-2097, 1983

A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for

A:Accession: A00914

A:Molecule type: mRNA

A:Residues: 8-163, 'N', 165-622 <DE2>

A:Cross-references: GB:V00595; GB:U00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344

A:Accession: B00914

A:Molecule type: DNA

A:Residues: 188-311 <DE3>

R:Malz, D.A.; Hewett-Ewmett, D.; Seegers, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74, 1968-1972, 1977

A:Reference number: A37549; MUID:77193964; PMID:266717

A:Accession: A37549

A:Molecule type: Protein

A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308,

R:Butkowsk, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.

A:Reference number: A37550; MUID:77207112; PMID:873923

A:Accession: A37550

A:Molecule type: Protein

A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 J. Biol. Chem. 261, 13210-13215, 1986
 A:Reference number: A37551; MUID:87008532; PMID:3759558

A:Contents: annotation: activation cleavages
 R:MacGillivray, R.T.; Irwin, D.M.; Guinot, E.R.; Stone, J.C.
 Ann. N.Y. Acad. Sci. 485, 79-79, 1986

A:Title: Recombinant genetic approaches to functional mapping of thrombin.

A:Reference number: I51952; MUID:87182874; PMID:3471151

A:Accession: I51952

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2, 'RI', 5-100 <RES>

A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin

C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds

ter 314-Arg, are released in natural blood clotting.

C:Comment: The gamma-carboxyglutamate residues bind calcium ions, result from the carboxy

ent interaction with the negatively charged phospholipid membrane surface.

C:Comment: The prothrombin precursor is synthesized in the liver.

C:Genetics:

A:Gene: GDB:F2

A:Map position: 11p11-11q12

A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 555/

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C:Keywords: acute phase; blood coagulation; calcium binding; carboxylglutamic acid; dupl

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-43/Domain: propeptide #status predicted <PRO>

F:28-87/Domain: Gla domain homology <Gla>

F:44-622/Product: prothrombin #status experimental <MNT>

F:108-186/Domain: kringle homology <KR1>

F:328-363/Product: thrombin light chain #status experimental <LCH>

F:364-622/Product: thrombin heavy chain #status experimental <HCH>

F:364-613/Domain: trypsin homology <TRY>

F:48,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:60,63,90-103,108-186,129-161,151-181,213-291,234-274,282-286/Disulfide bonds: #status

F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted

F:336-482,536-550,564-594/Disulfide bonds: #status predicted

F:391-407/Disulfide bonds: #status experimental

F:406,462/Active site: His, Asp #status predicted

F:416/Binding site: carboxylate (Asn) (covalent) #status experimental

F:568/Active site: Ser #status experimental

Query Match 45.8%; Score 87; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred. No. 2.4e-07;
 Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXLRBGSGLKRCXKXLCSPFXAFIFRNKXRTQFWVS 44
 Db 44 ANFLKEVRKGNLERECVEETCSYEAFALSTSTADVWAKY 87

RESULT 13

KFBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N:Alternate names: Christmas factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999

C:Accession: A14757; B20274; I55931; A00923

R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; T

Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979

A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas f

A:Reference number: A14757; MUID:8005619; PMID:291916

A:Accession: A14757

A:Molecule type: Protein

A:Residues: 1-63, 'T', 65-416 <KAT>

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood c

A:Reference number: A20274; MUID:83308813; PMID:668526

A:Accession: B20274

A:Molecule type: Protein

A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOB>
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A>Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A22673; PMID:85190593; PMID:3857619
A:Accession: A22673
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <MCG>
A:Cross-references: GB:M1309; NID:G180552; PIDN:AAA52023.1; PID:G180553
A>Note: the authors translated the codon ACG for residue 29 as Tyr
R:Joye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Pindel, A.; Tolstoch
Nucleic Acids Res. 11, 2325-2335, 1983
A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; PMID:83320788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <JAY>
A:Cross-references: GB:J00137; NID:G182610; PIDN:AAA52763.1; PID:G182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; PMID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M35672
R:Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A>Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; PMID:83065193; PMID:6595130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
A:Cross-references: GB:J00136; NID:G182608; PIDN:AAA58726.1; PID:G182609
R:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A>Title: Development of an immunofluorescent process for factor IX purification.
A:Reference number: A60486; PMID:90194857; PMID:2216207
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
R:McMullen, B.A.; Fujikawa, K.; Kiesel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; PMID:83308813; PMID:6688526
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109, 'X', 111-115 <MCM>
R:Balland, A.; Faure, T.; Carralio, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
Eur. J. Biochem. 172, 565-572, 1988
A>Title: Characterisation of two differently processed forms of human recombinant factor
A:Reference number: S02527; PMID:8816735; PMID:3380312
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAU>
A>Note: processed forms expressed in recombinant system
R:Julliat, S.; Petrucci, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien,
EMBO J. 9, 3295-3301, 1990
A>Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
A:Reference number: S12058; PMID:91006024; PMID:2209546
A:Accession: S12058
A:Molecule type: mRNA; protein
A:Residues: 1-68 <JAL>
A>Note: processed forms expressed in recombinant system
R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
EMBO J. 9, 475-480, 1990
A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
A:Reference number: S12377; PMID:90151623; PMID:2406129
A:Accession: S12377
A:Molecule type: protein

A:Residues: 92-130 <HAN>
A>Note: NMR detection of calcium binding by domain expressed in recombinant system
R:de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,
Thromb. Haemost. 70, 370-371, 1993
A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi
A:Reference number: I59612; PMID:94054330; PMID:8236150
A:Accession: I59612
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 444-461 <RES>
A:Cross-references: GB:S66752; NID:G439773; PIDN:AA82858.1; PID:G439774
R:Stotler, E.S.; Koerber, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A>Title: Genomic amplification with transcript sequencing.
A:Reference number: I59529; PMID:88127096; PMID:3340835
A:Accession: I59529
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 290-359 <RES>
A:Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomura, H.; Iw
Biochemistry 33, 5167-5171, 1994
A>Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
A:Reference number: A54255; PMID:94227047; PMID:8172892
A:Accession: A54255
A:Molecule type: protein
A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
A>Note: the residues designated 'X' were determined to be threonine bound to carbohydrat
R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A>Title: Activation of human factor IX (Christmas factor).
A:Reference number: A18483; PMID:78194509; PMID:659613
A:Contents: annotation; activation; active site; carboxydrate binding
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Am. Soc. Hematol. Abstr. 64(suppl.1), 262a, 1984
A:Reference number: A37563
A:Contents: annotation
A>Note: 194-Thr was also found
R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
A:Reference number: A37543; PMID:84185715; PMID:6425896
A:Contents: annotation; calcium binding
R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A:Reference number: A37544
A:Contents: annotation; calcium binding; correction
R:Benley, A.K.; Rees, D.O.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation
A:Reference number: A37545; PMID:86189947; PMID:3009023
A:Contents: annotation; signal sequence cleavage site
R:Suenhiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
J. Biol. Chem. 264, 2157-2165, 1989
A>Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by cryptoph
A:Reference number: A30622; PMID:90078229; PMID:2592373
A:Contents: annotation; sequence of mutant BIM
A>Note: carboxylation, glycosylation, and cleavage sites
R:Baron, M.; Notman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
submitted to the Brookhaven Protein Data Bank, November 1991
A:Reference number: A51252; PDB:1IXA
A:Contents: annotation; conformation; (1)H-NMR, residues 92-130
A>Note: recombinant form expressed in yeast
C:Comment: Factor IX is activated by factor xia, which excises the activation peptide pr
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C:Genetics:
A:Gene: GDB:P9
A:Cross-references: GDB:119900; OMIM:306900
A:Map position: Xq27.1-Xq27.2
A:Introns: 30/1, 84/2, 93/1, 131/1, 174/1, 241/3, 280/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

N:Alternate names: Stuart factor
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text change 16-Jul-1999
 C:Accession: A22867, #sequence, revision 17-Mar-1987 #text change 16-Jul-1999
 R:Funf, M.R.; Campbell, R.M.; MacGillivray, T.A.
 A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A:Reference number: A22867, MUID:84247315; PMID:6330671
 A:Accession: A22867
 A:Molecule type: mRNA
 A:Residues: 1-487 <RNA>
 A:Cross-references: GB:X00673; NID:9192; PIDN:CA55286.1; PID:9193
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry, 19, 659-667, 1980
 A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A:Reference number: A14997, MUID:80130563; PMID:6766735
 A:Accession: A14997
 A:Molecule type: protein
 A:Residues: 41-102, 'N', 104-180 <ENF>
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor X.
 A:Reference number: A20274, MUID:83308813; PMID:6688526
 A:Contents: annotation; revision to residue 103
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A:Reference number: A12030, MUID:76053069; PMID:1059093
 A:Accession: A12030
 A:Molecule type: protein
 A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKEG', 446-492 <T>
 R:Persson, E.; Selander, M.; Linde, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A:Reference number: A34412, MUID:89380326; PMID:2789221
 A:Accession: A34412
 A:Molecule type: protein
 A:Residues: 85-126 <PER>
 R:Morita, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A:Reference number: S39414, MUID:94062825; PMID:8243461
 A:Accession: S39414
 A:Molecule type: protein
 A:Residues: 183-196, 199-209, 216-233 <INO>
 A:Note: carbohydrate binding sites
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian
 A:Reference number: A12453, MUID:73053314; PMID:4264286
 A:Contents: annotation; active site
 R:Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to
 A:Reference number: A13504, MUID:76053121; PMID:1059122
 A:Contents: annotation; activation
 R:Stigo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A:Reference number: A38024, MUID:84185716; PMID:6546930
 A:Contents: annotation; calcium binding
 R:Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A:Reference number: A38025, MUID:86140210; PMID:3949800
 A:Contents: annotation; sulfate binding
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C:Comment: The two chains are formed from a single-chain precursor by the excision of two
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), and
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Genetics:
 A:Gene: F10
 A:Map position: 13q34
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <Gla>
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-233/Domain: activation peptide #status experimental <APT>
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F:234-461/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:200/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
 F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 46.8% Score 89; DB 1; Length 492;
 Best Local Similarity 36.4% Pred No 8 6e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCXXLCSEFXAFLFRXXRTQFWVS 44
 Db 41 ANSLFEVKGQNRERLEBACSLERAEVFEDEAEGDEFSKY 84

RESULT 11
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N:Alternate names: antihemophilic factor B; Christmas factor
 C:Species: Homo sapiens (man)
 C>Date: 17-Dec-1982 #sequence, revision 30-Jun-1997 #text change 15-Sep-2000
 C:Accession: A00922, A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20
 R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A:Reference number: A00922, MUID:86000558; PMID:2994716
 A:Accession: A00922
 A:Molecule type: DNA
 A:Residues: 1-461 <YOS>
 A:Cross-references: GB:K02402; NID:9182612; PIDN:AAB59620.1; PID:9182613
 R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Glanville, F.; Gould, K.; Huddleston, J.A.; Brc
 EMBO J. 3, 1053-1060, 1984
 A>Title: The gene structure of human anti-haemophilic factor IX.
 A:Reference number: A37570; MUID:84236100; PMID:6329734
 A:Accession: A37570
 A:Molecule type: DNA
 A:Residues: 1-461 <ANS>
 A:Cross-references: GB:K02048
 R:Reitma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A:Reference number: A30511; MUID:88327116; PMID:3416069
 A:Accession: A30511
 A:Molecule type: DNA
 A:Residues: 8-24 <REI>
 A:Cross-references: EMBL:X55008; NID:9311288; PIDN:CA539245.2; PID:94469253
 R:Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A:Reference number: A32989; MUID:89371752; PMID:2773937
 A:Accession: A32989

A:Accession: A25426
A:Molecule type: DNA
A:Residues: 1-445, 'L', 446-461 <PLU>
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R:Poster, D.; Dave, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A:Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781, MUID:84272714, PMID:6589653
A:Accession: A21781
A:Molecule type: mRNA
A:Residues: 'Q', 107-461 <FOS2>
A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
R:Beckmann, R.U.; Schmidt, R.U.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and its activation.
A:Reference number: A23789, MUID:85269639, PMID:2991859
A:Accession: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
R:Milietich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation in the presence of factor Va is not affected.
A:Reference number: A44605, MUID:50293094, PMID:1654179
A:Contents: annotation; carbohydrate binding sites; activation peptide
A:Note: The alpha form of protein C is glycosylated at Asn-329, and the beta form is not.
R:Harrie, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor C.
A:Reference number: A44606, MUID:92184750, PMID:1544894
A:Contents: annotation; beta-hydroxyaspartic acid
A:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that inactivation of factor Va is strongly enhanced by complexing with protein S. Protein C also functions as a single chain precursor, which is activated to a single chain active form.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is activated to a single chain active form.
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.
C:Genetic8:
A:Gene: GDB:PROC
A:Cross-references: GDB:120317; OMIM:176860
A:Map position: 2q13-2q21
A:Intons: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C1q domain homology; beta-hydroxyaspartic acid; blood coagulation; calcium binding
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
E:1-32/Domain: signal sequence #status predicted <SIG>
E:27-86/Domain: Gla domain homology <Gla>
E:33-42/Domain: propeptide #status predicted <PRO>
E:43-197/Product: protein C light chain #status predicted <LCH>
E:92-113/Domain: EGF homology <EG1>
E:140-175/Domain: EGF homology <EG2>
E:200-461/Product: protein C heavy chain #status predicted <HCH>
E:200-211/Domain: activation peptide #status experimental <APT>
E:212-445/Domain: trypsin homology <TRY>
E:48-49, 56-58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
E:59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/E
E:106-111/Disulfide bonds: #status predicted
E:110/Binding site: carbohydrate (Thr) (covalent) #status absent
E:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
E:139, 280, 355/Binding site: carbohydrate (Asn) (covalent) #status experimental
E:211-212/Ligand site: Arg-Leu (thrombin) #status experimental
E:253, 299, 402/Active site: His, Asp, Ser #status predicted
E:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

C/Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #ext_change 08-Dec-2000
 C/Accession: S49075; J04670; P50191; P50190; 162745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra-
 A/Reference number: A58498; MUID:96093366; PMID:8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <ST1>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; MUID:96194815; PMID:8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <ST1>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Experimental source: Cos-1 cell
 R/Enjoly, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A/Title: Characterization of rat factor X and Xa: demonstration of factor Xa in rat plasma
 A/Reference number: P50190; MUID:92041742; PMID:1718949
 A/Accession: P50191
 A/Molecule type: protein
 A/Residues: 41-58 'X', 60-65 <ENJ1>
 A/Accession: P50190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: 146196; MUID:94222160; PMID:8168596
 A/Accession: 162745
 A/Molecule type: DNA
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 295-383 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor Xa
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-119/Product: coagulation factor X light chain #status predicted <LCH>
 F:90-121/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-331/Domain: activation peptide #status predicted <ACT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-460/Domain: trypsin homology <TRY>
 F:46,47,54,55,59,60,65,66,67,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.9%; Score 93; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 1.6e-08;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

1 ANGFLXLDREGSLKRXCRXXLCSFFXAFIFPNXXRTQFWNSY 44
 41 ANSPFEETKGNLRECEVBEICSFEEAEVPEVDNKTETFPNNKY 84

RESULT 8

EXDU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N/Alternate names: Stuart factor
 C/Species: Homo sapiens (man)
 C/Date: 15-Nov-1984 #sequence_revision 02-May-1994 #ext_change 08-Dec-2000
 C/Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00
 R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A/Title: Gene for human factor X: a blood coagulation factor whose gene organization is
 A/Reference number: A24478; MUID:87026600; PMID:3768336
 A/Accession: A24478
 A/Molecule type: DNA
 A/Residues: 1-488 <LEY>
 A/Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:9182831
 R/Messler, T.L.; Plattman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor Xa
 A/Reference number: J00917; MUID:91216473; PMID:1902434
 A/Accession: J00917
 A/Molecule type: mRNA
 A/Residues: 1-488 <MES>
 A/Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:9182390
 R/Mao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor
 A/Reference number: A42485; MUID:92218390; PMID:1313796
 A/Accession: A42485
 A/Molecule type: DNA
 A/Residues: 1-15 <MA>
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A/Reference number: A25853; MUID:86221713; PMID:3011603
 A/Accession: A25853
 A/Molecule type: mRNA
 A/Residues: 19-284 'E', 289-488 <KAU>
 A/Cross-references: GB:M22613; NID:9180335; PIDN:AAA51984.1; PID:9180336
 R/Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A/Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X
 A/Reference number: A22208; MUID:85216545; PMID:2582420
 A/Accession: A22208
 A/Molecule type: mRNA
 A/Residues: 13-441 'S', 443-488 <FUN>
 A/Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:9182841
 R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A/Title: Characterization of a cDNA coding for human factor X.
 A/Reference number: A21284; MUID:84222026; PMID:6587384
 A/Accession: A21284
 A/Molecule type: mRNA
 A/Residues: 13-284 'E', 289-488 <LEY>
 A/Cross-references: GB:K01886
 R/Mulliken, B.A.; Fujikawa, K.; Kistiel, W.; Sasegawa, T.; Howald, W.N.; Kwa, E.Y.; Wein-
 Biochemistry 22, 2875-2884, 1983
 A/Title: Complete amino acid sequence of the light chain of human blood coagulation factor X
 A/Reference number: A20362; MUID:83257207; PMID:6671167
 A/Accession: A20362
 A/Molecule type: protein
 A/Residues: 41-179 <MCW>
 R/Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39415
 A/Molecule type: protein
 A/Residues: 183-234 <INO>
 A/Note: glycosylation sites
 A/Note: identification and characterization of beta-hydroxyaspartic acid
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.


```
OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAFXIFRNXXRTROFWVS 44
|||||
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C/Accession: 146932
R/Brother, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A/Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A/Reference number: 146932; MUID:93190306; PMID:8383365
A/Accession: 146932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-443 <BRO>
A/Cross-references: GB:556300; NID:g266294; PID:g266295
A/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F/24-89/Domain: Gla domain homology <GLA>
F/89-120/Domain: EGF homology <EG2>
F/130-166/Domain: EGF homology <EG2>
F/192-425/Domain: trypsin homology <TRY>

Query Match 67.4%; Score 128; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 8.5e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAFXIFRNXXRTROFWVS 44
|||||
Db 40 ANFLLELRPGSLERCKEELCFEAREVFTSTERTKQFWITY 83
|||||

RESULT 3
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
KFH07
C/Species: Homo sapiens (man)
C/Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C/Accession: A28322; A23819; A31186; B31186; S63524
R/O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Insley, M.Y.; Hagen, F.S.; Murti
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A/Reference number: A28322; MUID:87260948; PMID:3037537
A/Accession: A28322
A/Molecule type: DNA
A/Residues: 1-466 <OHA>
A/Cross-references: GB:002933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R/Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A/Title: Characterization of a cDNA coding for human factor VII.
A/Reference number: A23819; MUID:86205965; PMID:3466420
A/Accession: A23819
A/Molecule type: mRNA
A/Residues: 1-466 <HAG>
A/Cross-references: GB:M13232; NID:g182799; PIDN:AAA8040.1; PID:g182801
R/Thim, L.; Bioern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A/Reference number: A90539; MUID:89088153; PMID:3264725
A/Accession: A31186
A/Molecule type: protein
A/Residues: 61-212 <THI>
A/Accession: B31186
A/Molecule type: protein
A/Residues: 213-466 <TH2>
R/Bjoern, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen
J. Biol. Chem. 266, 11051-11057, 1991
A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A/Reference number: A40529; MUID:91250411; PMID:1904059
A/Contents: annotation; carbohydrate binding sites
R/Pederson, E.; Pedersen, L.C.
```

```
Eur. J. Biochem. 234, 293-300, 1995
A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A/Reference number: S63524; MUID:96096752; PMID:8529655
A/Accession: S63524
A/Molecule type: protein
A/Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C/Genetics:
A/Gene: GDB:F7
A/Cross-references: GDB:119897; OMIM:227500
A/Map position: 13q34-13q34
A/Insertions: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C/Function:
A/Description: catalyzes the proteolytic activation of coagulation factor X in the prese
oagulation factor IX in the presence of calcium and tissue factor
A/Pathway: blood coagulation extrinsic pathway
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-60/Domain: propeptide #status predicted <PRO>
F/45-104/Domain: Gla domain homology <GLA>
F/61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F/110-141/Domain: EGF homology <EG1>
F/151-187/Domain: EGF homology <EG2>
F/213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F/213-447/Domain: trypsin homology <TRY>
F/66,67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F/77-82,110-121,115-130,132-131,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F/112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental
F/123/Modified site: carboxy-beta-hydroxyaspartic acid (Asp) #status absent
F/205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/212-213/Cleavage site: Arg-ile (coagulation factor XIII) #status experimental
F/253,302,404/Active site: His, Asp, Ser #status predicted
F/350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 63.2%; Score 120; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAFXIFRNXXRTROFWVS 44
|||||
Db 61 ANFLLELRPGSLERCKEELCFEAREVFTSTERTKQFWISY 104
|||||

RESULT 4
protein C (activated) (EC 3.4.21.69) precursor - mouse
JX0210
N/Alternate names: vitamin K-dependent serine proteinase
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JX0210
R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A/Title: Isolation and characterization of a mouse protein C cDNA.
A/Reference number: JX0210; MUID:92316897; PMID:1618739
A/Accession: JX0210
A/Molecule type: mRNA
A/Residues: 1-461 <TAD>
A/Cross-references: GB:010445; NID:g220385; PIDN:BA01235.1; PID:g220386
A/Experimental source: liver
C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg
B.
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F/1-33/Domain: signal sequence #status predicted <SIG>
F/37-85/Domain: Gla domain homology <GLA>
F/34-41/Domain: propeptide #status predicted <PRO>
F/42-196,199-461/Product: protein C #status predicted <PNC>
F/42-196,199-461/Product: protein C #status predicted <PNC>
F/91-136/Domain: light chain #status predicted <LCU>
F/139-174/Domain: EGF homology <EG1>
F/139-461/Domain: heavy chain #status predicted <PCH>
F/199-211/Domain: activation peptide #status predicted <ACT>
F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28PHE_4
Perfect score: 190
Sequence: 1 ANGFLXLLREGSLKRXCRXX.....XXAFXIFRNXXRQRFWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	77.9	407	1 KFB07	coagulation factor
2	128	67.4	443	2 I46932	coagulation factor
3	120	63.2	466	1 KFH07	coagulation factor
4	104	54.7	461	1 UX0210	protein C (activat
5	103	54.2	461	1 S18994	protein C (activat
6	94	49.5	456	1 KXBO	coagulation factor
7	93	48.9	482	1 EXRT	coagulation factor
8	93	48.9	488	1 EXHU	coagulation factor
9	89	46.8	461	1 KXHU	protein C (activat
10	89	46.8	492	1 EXBO	coagulation factor
11	87	45.8	461	1 KFHU	coagulation factor
12	87	45.8	622	1 TBHU	thrombin (EC 3.4.2
13	85	44.7	416	1 KFB0	coagulation factor
14	84	44.2	617	2 S10511	thrombin (EC 3.4.2
15	84	44.2	618	2 A35827	thrombin (EC 3.4.2
16	81	42.6	475	1 EXCH	coagulation factor
17	80	42.1	452	1 A30351	coagulation factor
18	80	42.1	459	2 J00419	coagulation factor
19	78	41.1	625	1 TBBO	thrombin (EC 3.4.2
20	74	38.9	642	2 S53433	plasma protein S p
21	69	36.3	422	1 KXHUZ	plasma protein Z p
22	69	36.3	642	2 S53434	plasma protein S p
23	69	36.3	675	1 KXBOZ	plasma protein S p
24	69	36.3	675	1 KXBOZ	plasma protein S p
25	68	35.8	646	2 S18819	plasma protein S -
26	68	34.7	675	1 KXRS	plasma protein S p
27	65	34.2	396	1 KXBOZ	plasma protein Z -
28	59	31.1	675	1 KXMS	plasma protein S p
29	58	30.5	678	2 B48089	growth arrest-spec

30	57	30.0	673	2 A48089	growth arrest-spec
31	55	28.9	674	2 I55476	growth potentialin
32	52	27.4	605	1 MWLEB	E1 protein - bovin
33	52	27.4	620	1 MWLB2	E1 protein - bovin
34	48.5	25.5	2133	2 T42763	coagulation factor
35	48	25.3	413	1 VHVNH	nucleoprotein - in
36	46.5	24.5	594	2 D84859	probable MAP kinase
37	46.5	24.5	603	2 C96575	probable MAP kinase
38	45.5	23.9	576	2 G96763	probable MAP kinase
39	45	23.7	448	2 T18710	hypothetical prote
40	45	23.7	687	2 T08528	probable DNA topoi
41	44.5	23.4	304	2 AP2942	5-dehydro-4-deoxy
42	44.5	23.4	304	2 D96340	5-dehydro-4-deoxy
43	44	23.2	2351	1 E2HU	coagulation factor
44	43	22.6	536	1 E70066	hypothetical prote
45	43	22.6	1171	2 T31635	hypothetical prote

ALIGNMENTS

RESULT 1

KFB07

coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-May-1990 #sequence__revision 23-Mar-1995 #text__change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:83308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new triasaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

A:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F:1-44/Domain: Gla domain homology (fragment) <GDA>

F:50-81/Domain: EGF homology <EG1>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:152/Binding site: carbohydrate (Ser) (covalent) #status experimental

F:53/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment

F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-1le (coagulation factor XIIIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 77.9%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 2,1e-18;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 60 /note= "O-glycosylated"
FT Modified-site 145 /note= "O-glycosylated"
FT Modified-site 152..153 /note= "N-glycosylated"
FT Cleavage-site /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
FT WO200158935-A2.
PN
XX
XX 16-AUG-2001.
PD
XX
XX 12-FEB-2001; 2001WO-DK00094.
PR
XX 11-FEB-2000; 2000DK-0000218.
PR 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
PA
XX
PI Andersen KV, Pedersen AH, Bornaaes C;
XX
XX WPI; 2001-581807/65.
DR N-PSDB; AA199982.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX
PS Claim 1; Page 81-83; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration
CC between injections.
XX
SQ Sequence 406 AA;
Query Match 63.2%; Score 120; DB 22; Length 406;
Best Local Similarity 75.0%; Pred. No. 1,1e-11;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLLXLRGSLRXCRXXLCSPXXAPXIFRNXXRTPQWVS Y 44
DB 1 ANAFLLXLRGSLRXCRXXLCSPXXAPXIFRNXXRTPQWVS Y 44

Search completed: March 19, 2003, 14:51:15
Job time : 31.4375 secs

FT /note= "proteolytic site"
 FT 396..397
 FT /note= "proteolytic site"
 FT 402..403
 FT /note= "proteolytic site"
 FT
 PN USS580560-A.
 XX
 PD 03-DEC-1996.
 XX
 PP 13-NOV-1989; 89US-0434149.
 XX
 PR 09-AUG-1993; 93US-0104509.
 PR 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0898248.
 PR 22-AUG-1994; 94US-0293778.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
 PI WPI; 1997-033523/03.
 DR
 XX Mutated human factor VII or VIIa proteins - with amino acid
 PT substitutions to improve proteolytic stability
 PT
 XX Example 4; Page -: 28pp; English.
 PS
 CC Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.
 CC
 XX
 SQ Sequence 406 AA;

Query Match 63.2%; Score 120; DB 18; Length 406;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRGSLXRCXXLCSPFXAIFRNXXRTQFWVSY 44
 1 ANAFLELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 44
 Db

RESULT 14
 AAU77745
 ID AAU77745 standard; protein; 406 AA.
 XX
 AC AAU77745;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human factor VIIa active site mutant.
 XX
 KM Factor VIIa; human; shock heat treatment; protein stability;
 KM protein manufacture; protein conformation; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 193
 FT Active-site /note= "Member of the factor VIIa catalytic triad"
 FT Active-site 242
 FT /note= "Member of the factor VIIa catalytic triad"
 FT Active-site 344
 FT /note= "Member of the factor VIIa catalytic triad"

FT Misc-difference 344
 FT /label= Gly, Met, Thr
 FT /note= "Preferably Ala. Wild type Ser"
 FT
 PN WO200177141-A1.
 XX
 PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-DK00234.
 XX
 PR 06-APR-2000; 2000DK-0000573.
 PR 17-APR-2000; 2000US-197650P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PI Mathiesen F;
 PI WPI; 2001-657162/75.
 DR
 XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
 PT involves a shock heat treatment -
 PT
 XX Disclosure; Page -: 22pp; English.
 PS
 CC The invention describes a method of stabilising a polypeptide involving
 CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition, in the industrial or large scale method of
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified
 CC human factor VIIa protein, mutated at the catalytic site, described
 CC in the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been obtained using information given in the invention.
 CC
 XX
 SQ Sequence 406 AA;

Query Match 63.2%; Score 120; DB 22; Length 406;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRGSLXRCXXLCSPFXAIFRNXXRTQFWVSY 44
 1 ANAFLELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 44
 Db

RESULT 15
 AAM52171
 ID AAM52171 standard; Protein; 406 AA.
 XX
 AC AAM52171;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII SEQ ID NO 1.
 XX
 KM Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KM cardiant; hepatocrophic; cerebroprotective; haemophilia; liver disease;
 KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
 XX
 OS Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 6
 FT Misc-difference /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"

FT	Modified-site	322	/note= "glycosylation site"
FT	Dienulfide-bond	340..368	
FT	Cleavage-site	341..342	/note= "proteolytic site"
FT	Cleavage-site	392..393	/note= "proteolytic site"
FT	Cleavage-site	396..397	/note= "proteolytic site"
FT	Cleavage-site	402..403	/note= "proteolytic site"
XX			
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	13-NOV-1989;	89US-0434149.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
P1	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
DR	WPI, 1997-033523/03.		
XX			
PT	Mutated human factor VII or VIIA proteins - with amino acid		
FT	substitutions to improve proteolytic stability		
XX			
PS	Example 3; Page -: 28pp; English.		
XX			
CC	Modified human factor VII or VIIA proteins are stabilised against		
CC	proteolytic cleavage by substitution of one of the residues Lys32,		
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg315, Tyr332 and		
CC	Lys341 by an amino acid that provides a proteolytically more stable		
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,		
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating		
CC	bleeding disorders such as thrombocytopenia and von Willebrand's		
CC	disease. They are also suitable for addition to plasma substitutes.		
CC	The present sequence is a specific example of a modified factor VII		
protein.			
XX			
SQ	Sequence 406 AA:		
	Query Match 63.2%; Score 120; DB 18; Length 406;		
	Best Local Similarity 52.3%; Pred. No. 1.1e-11;		
	Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;		
OY	1 ANGFLXLRGSLRXCRXXLCSFXKAFIPFNXXXRTROFWISY 44		
	: :: : :		
Db	1 ANAFLELRPGSLERBCKEQQCSFEFARERIFDAERTKLFWISY 44		
RESULT 13			
AAM14510			
ID	AAM14510 standard; protein; 406 AA.		
XX			
AC	AAM14510;		
XX			
DT	14-MAY-1997 (first entry)		
XX			
DE	Modified blood coagulation Factor VII (R315S).		
XX			
KW	Blood coagulation; factor 7; mutein; mutation; modification;		
XX	thrombocytopenia; von Willebrand's disease; plasma substitute.		
OS	Homo sapiens.		
CS	Synthetic.		
XX			
PH	Key Location/Qualifiers		

FT	Modified-site	6	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	7	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	14	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	16	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	19	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	20	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	17..22	/note= "gamma-carboxyglutamic acid"
FT		25	/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"	
FT		26	/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"	
FT		29	/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"	
FT		32..33	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	/note= "proteolytic site"	
FT		35	/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"	
FT		38..39	/note= "proteolytic site"
FT	Cleavage-site	42..43	/note= "proteolytic site"
FT		44..45	/note= "proteolytic site"
FT	Cleavage-site	50..61	/note= "proteolytic site"
FT		55..70	/note= "proteolytic site"
FT	Modified-site	63	/label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Disulfide-bond	72..81	/note= "beta-hydroxy-aspartic acid"
FT		91..102	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	98..112	/note= "beta-hydroxy-aspartic acid"
FT		114..127	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	135..162	/note= "beta-hydroxy-aspartic acid"
FT		143..144	/note= "beta-hydroxy-aspartic acid"
FT	Cleavage-site	145	/note= "beta-hydroxy-aspartic acid"
FT		159..164	/note= "beta-hydroxy-aspartic acid"
FT	Modified-site	178..194	/note= "beta-hydroxy-aspartic acid"
FT		193	/note= "beta-hydroxy-aspartic acid"
FT	Active-site	242	/note= "beta-hydroxy-aspartic acid"
FT		290..291	/note= "beta-hydroxy-aspartic acid"
FT	Active-site	310..329	/note= "beta-hydroxy-aspartic acid"
FT		315..316	/note= "beta-hydroxy-aspartic acid"
FT	Cleavage-site	315	/note= "beta-hydroxy-aspartic acid"
FT		315	/note= "beta-hydroxy-aspartic acid"
FT	Misc-difference	315	/note= "beta-hydroxy-aspartic acid"
FT		322	/note= "beta-hydroxy-aspartic acid"
FT	Modified-site	340..368	/note= "beta-hydroxy-aspartic acid"
FT		341..342	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	392..393	/note= "beta-hydroxy-aspartic acid"
FT		392..393	/note= "beta-hydroxy-aspartic acid"

```

FH Key Location/Qualifiers
FT Region 1..152
FT /note="Factor VII light chain"
FT Region 153..406
FT /note="Factor VII heavy chain"
FT Peptide 374..388
FT /note="exosite 1"
FT Peptide 290..310
FT /note="exosite 2"
FT Peptide 290..310
FT /note="pref. PC polypeptide; claim 2, page 136"
FT Peptide 374..388
FT /note="pref. PC polypeptide; claim 2, page 136"
FT Peptide 289..304
FT /note="pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..304
FT /note="pref. PC polypeptide; claim 4, page 137"
FT Peptide 245..266
FT /note="claim 9, page 138-139 describes an antibody
that reacts with Factor VII; fragments
289-304, 290-304, 290-310, 374-388 and
400-414 but not with fragment 245-266"
FT Peptide
FT WO9309804-A.
PN 27-MAY-1993.
PD 18-NOV-1992; 92WO-US10242.
XX 18-NOV-1991; 91US-0793989.
PR (SCRI ) SCRIpps RES INST.
XX (SCRI ) SCRIpps RES INST.
PI Griffin JH, Mesters RM;
XX WPI; 1993-182244/22.
XX DR
XX Serine protease derived-polypeptide(s) and anti-peptide
PT antibodies - for inhibiting coagulation and assaying for the
PT presence of serine protease in fluid samples
XX
XX PS Disclosure; Page 133-135; 149pp; English.
XX CC The PC polypeptides indicated in the Features Table inhibit
CC coagulation (they prevent binding of serine protease to natural
CC substrates), esp. when admin. to give an intravascular blood
CC concn. of 0.1-100 (pref. 0.5-10) microm.
CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
CC in the specification but have not yet been added to the SEQUENCE
CC LISTING.
XX
XX SQ Sequence 406 AA;
Query Match 63.2%; Score 120; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 1 ANGFLXALREGSLKRCXKXLCSPFXAFIRNXXRTQFWVS 44
1 ANAFLELRPGSLRECKECCSFEARERFDKARTLFWISY 44
Db
RESULT 12
AAW14509
ID AAW14509 standard; protein; 406 AA.
XX
XX AAW14509;
AC
XX 14-MAY-1997 (first entry)
DT
XX Modified blood coagulation Factor VII (R290S).
DB
XX Modified blood coagulation; factor 7; mutain; mutation; modification;
KW

```

```

KW Thrombocytopenia; von Willebrand's disease; plasma substitute.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 14
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 16
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 19
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 20
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Disulfide-bond 17..22
FT /note="gamma-carboxylutamic acid"
FT Modified-site 25
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 26
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 29
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Modified-site 32..33
FT /note="gamma-carboxylutamic acid"
FT Modified-site 35
FT /label= OTHER
FT /note="gamma-carboxylutamic acid"
FT Cleavage-site 38..39
FT /note="proteolytic site"
FT Cleavage-site 42..43
FT /note="proteolytic site"
FT Cleavage-site 44..45
FT /note="proteolytic site"
FT Disulfide-bond 50..61
FT /note="proteolytic site"
FT Modified-site 63
FT /label= OTHER
FT /note="beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81
FT /label= OTHER
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Disulfide-bond 143..144
FT /note="proteolytic site"
FT Modified-site 145
FT /note="glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note="proteolytic site in unmodified factor VII"
FT Misc-difference 290
FT /note="native Arg290 has been substituted by Ser to
provide a proteolytically more stable peptide
bond"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note="proteolytic site"

```

CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.

XX Sequence 44 AA;

Query Match 63.2%; Score 120; DB 22; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.4e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKXLCSPFXAFLFRNXXRTROPFWSY 44
 DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 9

ID AAB84870 standard; Protein; 401 AA.

AC AAB84870;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KM mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 31..317

FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"

FT JP2001061479-A.

PN 13-MAR-2001.

PD 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19463.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -

PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKXLCSPFXAFLFRNXXRTROPFWSY 44
 DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 10

AAB84871
 ID AAB84871 standard; Protein; 401 AA.

AC AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KM mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 235..239

FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 Asp-Arg-Lys-Thr-Leu"

FT Misc-difference 31..317

FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"

FT JP2001061479-A.

PN 13-MAR-2001.

PD 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -

PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKXLCSPFXAFLFRNXXRTROPFWSY 44
 DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 11

AAR35764
 ID AAR35764 standard; Protein; 406 AA.

AC AAR35764;

DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
 XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
 XX exosite; catalytic activity.

OS Homo sapiens.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10GLU28PHE_4
Perfect score: 190
Sequence: 1 ANGFLXLRREGSLRXRCRX.....XXAFXIFRNXXRQFWWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	81.6	44	20	AAV18306
2	155	81.6	44	22	AAV18306
3	129	67.9	44	20	AAV18312
4	126	66.3	44	20	AAV18310
5	123	64.7	44	20	AAV18311
6	121	63.7	44	20	AAV18302
7	120	63.2	44	20	AAV18305
8	120	63.2	44	22	AAV18305
9	120	63.2	401	22	AAV18305
10	120	63.2	401	22	AAV18305

11	120	63.2	406	14	AAV18306	Factor VII (VII).
12	120	63.2	406	18	AAV14509	Modified blood coa
13	120	63.2	406	18	AAV14510	Modified blood coa
14	120	63.2	406	22	AAV17745	Human factor VIIa
15	120	63.2	406	22	AAV52171	Human FVII SEQ ID
16	120	63.2	406	22	AAV52172	Mammalian exprese
17	120	63.2	406	22	AAV52181	Human FVII mutant
18	120	63.2	406	22	AAV52182	Human FVII mutant
19	120	63.2	406	22	AAV52183	Human FVII mutant
20	120	63.2	406	22	AAV52184	Human FVII mutant
21	120	63.2	406	22	AAV52185	Human FVII mutant
22	120	63.2	406	22	AAV52186	Human FVII mutant
23	120	63.2	406	22	AAV52187	Human FVII mutant
24	120	63.2	406	22	AAV52188	Human FVII mutant
25	120	63.2	406	22	AAV52189	Human FVII mutant
26	120	63.2	406	22	AAV52190	Human FVII mutant
27	120	63.2	406	22	AAV52191	Human FVII mutant
28	120	63.2	406	22	AAV52192	Human FVII mutant
29	120	63.2	406	22	AAV52193	Human FVII mutant
30	120	63.2	406	22	AAV52194	Human FVII mutant
31	120	63.2	406	22	AAV52195	Human FVII mutant
32	120	63.2	406	22	AAV52196	Human FVII mutant
33	120	63.2	406	22	AAV52197	Human FVII mutant
34	120	63.2	406	22	AAV52198	Human FVII mutant
35	120	63.2	406	22	AAV52199	Human FVII mutant
36	120	63.2	406	22	AAV52200	Human FVII mutant
37	120	63.2	406	22	AAV52201	Human FVII mutant
38	120	63.2	406	22	AAV52202	Human FVII mutant
39	120	63.2	406	22	AAV52203	Human FVII mutant
40	120	63.2	406	22	AAV52204	Human FVII mutant
41	120	63.2	406	22	AAV52205	Human FVII mutant
42	120	63.2	406	22	AAV52206	Human FVII mutant
43	120	63.2	406	22	AAV52207	Human FVII mutant
44	120	63.2	406	22	AAV52208	Human FVII mutant
45	120	63.2	406	22	AAV52209	Human FVII mutant

ALIGNMENTS

RESULT 1	AAV18306	standard, peptide, 44 AA.
ID	AAV18306	standard, peptide, 44 AA.
XX	AAV18306	standard, peptide, 44 AA.
AC	AAV18306	standard, peptide, 44 AA.
XX	AAV18306	standard, peptide, 44 AA.
DT	17-ANG-1999	(first entry)
XX	17-ANG-1999	(first entry)
DE	Bovine factor VII	GLA domain.
XX	Bovine factor VII	GLA domain.
KW	GLA domain; vitamin K-dependent protein; clotting disorder;	
XX	therapy.	
OS	Bos taurus.	
XX	Bos taurus.	
FH	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	FT	note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	W0920767-A1.	
XX	W0920767-A1.	
PD	29-APR-1999.	
XX	29-APR-1999.	
PF	20-OCT-1998;	98WO-US22152.
XX	20-OCT-1998;	98WO-US22152.
PR	23-OCT-1997;	97US-0955636.
XX	23-OCT-1997;	97US-0955636.
PA	(MINU) UNIV MINNESOTA.	
XX	(MINU) UNIV MINNESOTA.	
PI	Nelaeetuen GL;	
XX	Nelaeetuen GL;	
DR	WPI; 1999-288309/24.	

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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease;
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match: 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXRLREGSLRXRCRXLLCSFXXAEXIFRNXXTRTQFWY 44
DB 41 ANSFEEFKGNLERECMEICSYEVRRIFFEDDKTKYWKY 84

RESULT 9
ID 088947; PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; Pubmed=9684791;
RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MW; BAC09D5EF9D271E CRC64;

Query Match: 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXRLREGSLRXRCRXLLCSFXXAEXIFRNXXTRTQFWY 44
DB 41 ANSFEEFKGNLERECMEICSYEVRRIFFEDDKTKYWKY 84

RESULT 10
ID 014316; PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1999 (TRENBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX [Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B]) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RT Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; Pubmed=3416069;
RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemsma A.,
RA Brier E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; EGFBLDOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
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DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 47.6%; Score 90; DB 4; Length 456;
 Best Local Similarity 39.5%; Pred. No. 3.9e-08;
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLLREGSLKRXKXCLCSFYXAXEIRNXXRTQRFWVS 44
 DB 44 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFFWKQY 86

RESULT 11

Q95ND7 PRELIMINARY; PRT; 461 AA.

AC Q95ND7; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Coagulation factor XI.
 GN F9.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=504;
 RA Satta Y.;

"Comparison of DNA and protein polymorphisms between humans and
 RT chimpanzees.";

RL Gene Genet. Syst. 0:0-0(2001).
 DR EMBL; AB062470; BAB58885.1; JOINED.
 DR EMBL; AB062458; BAB58885.1; JOINED.
 DR EMBL; AB062460; BAB58885.1; JOINED.
 DR EMBL; AB062462; BAB58885.1; JOINED.
 DR EMBL; AB062464; BAB58885.1; JOINED.
 DR EMBL; AB062466; BAB58885.1; JOINED.
 DR EMBL; AB062468; BAB58885.1; JOINED.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; GGF_1.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 47.6%; Score 90; DB 6; Length 461;
 Best Local Similarity 39.5%; Pred. No. 3.9e-08;
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLLREGSLKRXKXCLCSFYXAXEIRNXXRTQRFWVS 44
 DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFFWKQY 91

RESULT 12

Q95ND6 PRELIMINARY; PRT; 461 AA.

AC Q95ND6; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Coagulation factor XI.
 GN F9.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=505;
 RA Satta Y.;

"Comparison of DNA and protein polymorphisms between humans and
 RT chimpanzees.";

RL Gene Genet. Syst. 0:0-0(2001).
 DR EMBL; AB062471; BAB58886.1; JOINED.
 DR EMBL; AB062459; BAB58886.1; JOINED.
 DR EMBL; AB062461; BAB58886.1; JOINED.
 DR EMBL; AB062463; BAB58886.1; JOINED.
 DR EMBL; AB062465; BAB58886.1; JOINED.
 DR EMBL; AB062467; BAB58886.1; JOINED.
 DR EMBL; AB062469; BAB58886.1; JOINED.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; GGF_1.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 47.6%; Score 90; DB 6; Length 461;
 Best Local Similarity 39.5%; Pred. No. 3.9e-08;
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLLREGSLKRXKXCLCSFYXAXEIRNXXRTQRFWVS 44
 DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFFWKQY 91

RESULT 13

Q9GMD9 PRELIMINARY; PRT; 469 AA.

AC Q9GMD9; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Coagulation factor X.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OC NCBI_TaxID=9258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21015017; PubMed=11132153;
 RA Poorafshar M., Aveskoeh M., Munday B., Hellman L.;

"Identification and structural analysis of four serine proteases in a

```
RT monocyte, the platypus, Ornithorhynchus anatinus."
RL Immunogenetics 52:19-28 (2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AF275654; AAC00453.1; -.
DR HSSP: P00742; 1XKB.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ
SEQUENCE 469 AA; 52196 MW; 4C66C23D0758F6A CRC64;

Query Match 47.1%; Score 89; DB 6; Length 469;
Best Local Similarity 34.1%; Pred. No. 6.1e-08;
Matches 15; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRGSLXRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
Db 41 ANSLFEELKKGNLERECNETCSYEAREVFEDTKTNEFWNTY 84

RESULT 14
Q9SME8 PRELIMINARY; PRT; 49 AA.
AC Q9SME8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN 11)
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF394598; AAK7556.1; -.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6023 MW; DISC6DE9CCBA4A14 CRC64;

Query Match 46.6%; Score 88; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 1e-08;
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Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRGSLXRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
Db 6 SGKLEFVRGNLERECKEKCSFEAREVFENTKTEFWKQY 48

RESULT 15
Q28994 PRELIMINARY; PRT; 138 AA.
AC Q28994;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Mature porcine factor IX (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN 11)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96003866; PubMed=7568220;
RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module
RT structure related to Xase activity and hemophilia B."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800 (1995).
RN 12)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lollar P.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51135; AAA96318.1; -.
DR HSSP: P00740; 1EDM.
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF-II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00010; EGFBLDOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15515 MW; 793B4BDE4D5FAFAD CRC64;

Query Match 42.9%; Score 81; DB 6; Length 138;
Best Local Similarity 41.2%; Pred. No. 5.7e-07;
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 11 GSLLXRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
Db 4 GNLERECIRKCSFEAREVFENTKTEFWKQY 37

Search completed: March 19, 2003, 15:13:36
Job time : 46.3125 secs
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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLU28GLU_4
Perfect score: 189
Sequence: 1 ANGFLXLRGSLXRCXCRX.....XXAEXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	82.5	44	3	US-08-955-636-4
2	129	66.3	44	3	US-08-955-636-26
3	126	65.7	44	3	US-08-955-636-27
4	124	65.6	44	3	US-08-955-636-30
5	123	65.1	44	3	US-08-955-636-3
6	123	65.1	406	1	US-08-293-778-24
7	123	65.1	406	1	US-08-295-411-5
8	123	65.1	406	1	US-08-955-471-5
9	123	65.1	406	5	PCT-US92-10242-5
10	123	65.1	444	1	US-08-475-845-2
11	123	65.1	444	2	US-08-327-690-2
12	123	65.1	444	2	US-08-660-289-2
13	123	65.1	444	2	US-08-537-807-2
14	123	65.1	444	2	US-08-871-003-2
15	123	65.1	444	3	US-08-464-233-2
16	123	65.1	444	4	US-09-189-607-2
17	123	65.1	444	4	US-09-378-907-2
18	123	65.1	444	5	PCT-US94-05779-2
19	123	65.1	466	1	US-07-882-202A-4
20	123	65.1	466	1	US-08-021-615A-4
21	123	65.1	466	4	US-08-321-777-4
22	123	65.1	466	4	US-09-009-217-14
23	123	65.1	466	4	US-09-009-656-14
24	123	65.1	466	5	PCT-US93-04493-4
25	120	63.5	44	3	US-08-955-636-28
26	119	63.0	44	3	US-08-955-636-29
27	109	57.7	41	1	US-08-229-280-4

28	101	53.4	139	1	US-08-330-978-2	Sequence 2, Appl1
29	101	53.4	139	1	US-08-474-042-2	Sequence 2, Appl1
30	101	53.4	139	1	US-08-484-558-2	Sequence 2, Appl1
31	101	53.4	139	1	US-08-774-592-2	Sequence 2, Appl1
32	101	53.4	437	1	US-08-487-037-2	Sequence 2, Appl1
33	101	53.4	437	1	US-08-487-037-2	Sequence 2, Appl1
34	101	53.4	488	1	US-08-487-037-1	Sequence 2, Appl1
35	98	51.9	44	3	US-08-955-636-23	Sequence 2, Appl1
36	98	51.9	44	3	US-08-955-636-35	Sequence 2, Appl1
37	97	51.3	44	3	US-08-955-636-2	Sequence 2, Appl1
38	96	50.8	448	1	US-08-295-411-3	Sequence 2, Appl1
39	96	50.8	448	2	US-08-955-471-3	Sequence 3, Appl1
40	96	50.8	448	5	PCT-US92-10068-1	Sequence 3, Appl1
41	96	50.8	448	5	PCT-US92-10242-3	Sequence 3, Appl1
42	95	50.3	44	3	US-08-955-636-24	Sequence 24, Appl1
43	93	49.2	41	1	US-08-229-280-5	Sequence 2, Appl1
44	93	49.2	42	2	US-08-745-254A-2	Sequence 2, Appl1
45	93	49.2	44	3	US-08-955-636-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      82.5%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ANGFLXLRGSLXRCXCRXLCSPFXAEXIFRNXXRTQFWVS 44
DB      1 ANGFLXLRGSLXRCXCRXLCSPFXAEXIFRNXXRTQFWVS 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129,224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-293-778-24

Query Match
Best Local Similarity 65.1%; Score 123; DB 1; Length 406;
Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLLXLRGSLRXRCRXLCSPXXAEXIFRNXXRTROFWISY 44
Db 1 ANAFLYLRPGSLRYCKYQCSFYARIYFDARTKLFWISY 44

RESULT 7
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Office of Patent Counsel, The Scripps
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match
Best Local Similarity 65.1%; Score 123; DB 1; Length 406;
Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLLXLRGSLRXRCRXLCSPXXAEXIFRNXXRTROFWISY 44
Db 1 ANAFLELRPGSLRERCKEQQCSFEARIRIFDARTKLFWISY 44

RESULT 8
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Office of Patent Counsel, The Scripps
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 65.1%; Score 123; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXXLCSEFXAEXIFRNXXRTROPFWVS 44
DB 1 ANAFLEBLRPGSLRECKEBCQCSFEERARLFXDAERIKLFWIS 44

RESULT 9
PCT-US92-10242-5

Sequence 5, Application PC/RUS9210242

GENERAL INFORMATION:

APPLICANT: Griffin, John H.

APPLICANT: Meesters, Rolf

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods

TITLE OF INVENTION: for Inhibiting Coagulation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Office of Patent Counsel, The Scripps

ADDRESSEE: Research Institute

STREET: 10666 North Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793,989

FILING DATE: 18-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 406 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: Region

LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"

FEATURE:

NAME/KEY: Region

LOCATION: 153..406

OTHER INFORMATION: /note= "Factor VII Heavy Chain"

PCT-US92-10242-5

Query Match 65.1%; Score 123; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 2.4e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXXLRGSLXRCXKXXLCSEFXAEXIFRNXXRTROPFWVS 44
DB 1 ANAFLEBLRPGSLRECKEBCQCSFEERARLFXDAERIKLFWIS 44

RESULT 10
US-08-475-845-2

Sequence 2, Application US/08475845

Patent No. 578965

GENERAL INFORMATION:

APPLICANT: Berkner, Kathleen L.

APPLICANT: Petersen, Lars C.

APPLICANT: Hart, Charles E.

APPLICANT: Hedner, Ulla

APPLICANT: Bregengaard, Claus

TITLE OF INVENTION: Modified Factor VII

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco

STATE: CA

COUNTRY: U.S.A.

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,845

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/327,690

FILING DATE: 24-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/065,725

FILING DATE: 21-MAY-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/662,920

FILING DATE: 28-FEB-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-845-2

Query Match 65.1%; Score 123; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXXLCSEFXAEXIFRNXXRTROPFWVS 44
DB 39 ANAFLEBLRPGSLRECKEBCQCSFEERARLFXDAERIKLFWIS 82

RESULT 11
US-08-327-690-2

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; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLEELRPGSLERCKEQCSFEAREIFPDARTKLFWISY 82

RESULT 12
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower

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; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLEELRPGSLERCKEQCSFEAREIFPDARTKLFWISY 82

RESULT 13
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-537-807-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
DB 39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWIS 82

RESULT 14
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Raasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-871-003-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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QY 1 ANGFLLXLRGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
DB 39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWIS 82

RESULT 15
US-08-464-233-2
; Sequence 2, Application US/08464233
; Patent No. 6039944
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-464-233-2

Query Match          65.1%; Score 123; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
DB 39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWIS 82

Search completed: March 19, 2003, 15:16:17
Job time : 9.75 secs
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GenCore version 5.1.4_p5 4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10GLU28GLU_4
Perfect score: 189
Sequence: 1 ANGFLXLRPGSLKRXCRXX.....XXAEXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	123	65.1	406	US-10-109-498-1	Sequence 1, Appli
2	95	50.3	419	US-10-182-263-6	Sequence 6, Appli
3	93	49.2	419	US-10-182-263-1	Sequence 1, Appli
4	93	49.2	419	US-10-182-263-3	Sequence 3, Appli
5	93	49.2	419	US-10-182-263-4	Sequence 4, Appli
6	93	49.2	419	US-10-182-263-5	Sequence 5, Appli
7	93	49.2	419	US-09-978-917A-4	Sequence 2, Appli
8	93	49.2	461	US-10-182-263-2	Sequence 2, Appli
9	93	49.2	461	US-09-978-917A-2	Sequence 2, Appli
10	90	47.6	415	US-09-118-748-2	Sequence 5, Appli
11	90	47.6	461	US-10-132-829-5	Sequence 3, Appli
12	90	47.6	461	US-09-884-901-3	Sequence 3, Appli
13	70	37.0	96	US-09-759-130B-313	Sequence 313, App
14	70	37.0	209	US-09-759-130B-110	Sequence 310, App
15	70	37.0	226	US-09-759-130B-110	Sequence 310, App
16	53	28.0	95	US-09-759-130B-356	Sequence 356, App
17	53	28.0	208	US-09-759-130B-355	Sequence 355, App
18	53	28.0	225	US-09-759-130B-353	Sequence 353, App
19	43	22.8	484	US-09-801-368-334	Sequence 334, App

20	42	22.2	233	10	US-09-867-550-1024	Sequence 1024, App
21	40.5	21.4	197	9	US-10-076-622-516	Sequence 516, App
22	40.5	21.4	197	12	US-10-007-805-516	Sequence 516, App
23	40.5	21.4	232	9	US-10-076-622-517	Sequence 517, App
24	40.5	21.4	232	12	US-10-007-805-517	Sequence 517, App
25	40.5	21.4	243	9	US-09-938-418-7	Sequence 7, Appli
26	40.5	21.4	243	9	US-10-045-992-4	Sequence 4, Appli
27	40.5	21.4	243	9	US-10-063-547-122	Sequence 122, App
28	40.5	21.4	243	9	US-10-174-590-366	Sequence 366, App
29	40.5	21.4	243	9	US-10-176-758-366	Sequence 366, App
30	40.5	21.4	243	9	US-10-063-616-122	Sequence 122, App
31	40.5	21.4	243	9	US-10-175-737-366	Sequence 366, App
32	40.5	21.4	243	9	US-10-063-502-122	Sequence 122, App
33	40.5	21.4	243	9	US-10-076-622-514	Sequence 514, App
34	40.5	21.4	243	9	US-10-173-706-366	Sequence 366, App
35	40.5	21.4	243	9	US-10-175-738-366	Sequence 366, App
36	40.5	21.4	243	9	US-10-175-752-366	Sequence 366, App
37	40.5	21.4	243	9	US-10-176-482-366	Sequence 366, App
38	40.5	21.4	243	9	US-10-176-757-366	Sequence 366, App
39	40.5	21.4	243	9	US-10-176-913-366	Sequence 366, App
40	40.5	21.4	243	9	US-10-180-552-366	Sequence 366, App
41	40.5	21.4	243	9	US-10-180-557-366	Sequence 366, App
42	40.5	21.4	243	9	US-10-173-700-366	Sequence 366, App
43	40.5	21.4	243	9	US-10-174-572-366	Sequence 366, App
44	40.5	21.4	243	9	US-10-174-579-366	Sequence 366, App
45	40.5	21.4	243	9	US-10-174-582-366	Sequence 366, App

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      65.1%, Score 123, DB 9, Length 406;
Best Local Similarity 75.0%; Pred. No. 1.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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QY 1 ANGFLXLRPGSLKRXCRXXCFXXAEXIFRNXXRTQFWVS 44
DB 1 ANAFLXLRPGSLKRXCRXXCFXXAEXIFRNXXRTQFWVS 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
```

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          50.3%; Score 95; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

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DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXRXLCSPFXAEXIFRNXXRTQFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFQNVDDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXRXLCSPFXAEXIFRNXXRTQFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXRXLCSPFXAEXIFRNXXRTQFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens
US-10-182-263-5

Query Match 49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 1 ANSFLEELRHSSLERECIEICDFEAKEIFQVDDTLAFW 41

RESULT 7
US-09-978-917A-4
Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978, 917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 1 ANSFLEELRHSSLERECIEICDFEAKEIFQVDDTLAFW 41

RESULT 8
US-10-182-263-2
Sequence 2, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182, 263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 43 ANSFLEELRHSSLERECIEICDFEAKEIFQVDDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978, 917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 43 ANSFLEELRHSSLERECIEICDFEAKEIFQVDDTLAFW 83

RESULT 10
US-09-118-748-2
Sequence 2, Application US/09118748A
Patent No. US20020031799A1
GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
TITLE OF INVENTION: Actively
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118, 748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053, 571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 47.6%; Score 90; DB 10; Length 415;
Best Local Similarity 39.5%; Pred. No. 7.4e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 44
DB 3 SGKLEEFVQGNLERBQMEKCSFEABAEVFENTERTEFWKQY 45

RESULT 11
US-10-132-829-5
Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
FILE REFERENCE: 6627-Pall70

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          47.6%; Score 90; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY      2 NGFLXXLREGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB      49 SGKLEEFVQGNLERECMEKCSFEAREVFEVNTERTTEFFWK 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18,902
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match          47.6%; Score 90; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY      2 NGFLXXLREGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB      49 SGKLEEFVQGNLERECMEKCSFEAREVFEVNTERTTEFFWK 91

RESULT 13
US-09-759-1308-313
; Sequence 313, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-313

Query Match          37.0%; Score 70; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 5.3e-05;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      11 GSIXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB      46 GNLERECNELCNVEAREIFVDEDDXTIAFWCEY 79

RESULT 14
US-09-759-1308-312
; Sequence 312, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-313
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match      37.0%; Score 70; DB 9; Length 209;
Best Local Similarity 38.2%; Pred. No. 0.00012;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      11  GSLKRXCRXXLCSPXXAEXIFRXRXRTROFWVSY 44
DB      46  GNLERCNEELCNVEEARREIFVDEKTIAPFQEXY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350NM1M
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match      37.0%; Score 70; DB 9; Length 226;
Best Local Similarity 38.2%; Pred. No. 0.00013;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      11  GSLKRXCRXXLCSPXXAEXIFRXRXRTROFWVSY 44
DB      63  GNLERCNEELCNVEEARREIFVDEKTIAPFQEXY 96
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Search completed: March 20, 2003, 13:30:15
Job time : 8.375 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10Gln28PHE
Perfect score: 191
Sequence: 1 ANAFLLXLRQSLXRCCKX.....XXAFIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: A Geneseq 101002: *
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT: *
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11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
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14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: *
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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.4	44	20	AAV18312
2	159	83.2	44	20	AAV18310
3	158	82.7	44	20	AAV18302
4	157	82.2	44	20	AAV18311
5	156	81.7	44	20	AAV18305
6	156	81.7	44	22	AAV18395
7	156	81.7	401	22	AAV18470
8	156	81.7	401	22	AAV18471
9	156	81.7	406	14	AAV15764
10	156	81.7	406	18	AAV14509

11	156	81.7	406	18	AAV14510	Modified blood coa
12	156	81.7	406	22	AAV77745	Human factor VIIA
13	156	81.7	406	22	AAV52171	Human FVII SEQ ID
14	156	81.7	406	22	AAV52182	Mammalian expresse
15	156	81.7	406	22	AAV52181	Human FVII mutant
16	156	81.7	406	22	AAV52182	Human FVII mutant
17	156	81.7	406	22	AAV52183	Human FVII mutant
18	156	81.7	406	22	AAV52184	Human FVII mutant
19	156	81.7	406	22	AAV52185	Human FVII mutant
20	156	81.7	406	22	AAV52186	Human FVII mutant
21	156	81.7	406	22	AAV52187	Human FVII mutant
22	156	81.7	406	22	AAV52188	Wild-type human bl
23	156	81.7	406	22	AAV52189	Mutant blood coagu
24	156	81.7	406	22	AAV52190	Mutant blood coagu
25	156	81.7	406	22	AAV52191	Mutant blood coagu
26	156	81.7	406	23	AAV52192	Human coagulation
27	156	81.7	406	23	AAV52193	Human coagulation
28	156	81.7	406	23	AAV52194	Human coagulation
29	156	81.7	406	23	AAV52195	Human coagulation
30	156	81.7	406	23	AAV52196	Human coagulation
31	156	81.7	406	23	AAV52197	Human coagulation
32	156	81.7	406	23	AAV52198	Human coagulation
33	156	81.7	406	23	AAV52199	Human coagulation
34	156	81.7	406	23	AAV52200	Human coagulation
35	156	81.7	406	23	AAV52201	Human coagulation
36	156	81.7	406	23	AAV52202	Human coagulation
37	156	81.7	406	23	AAV52203	Human coagulation
38	156	81.7	406	23	AAV52204	Human coagulation
39	156	81.7	406	23	AAV52205	Human coagulation
40	156	81.7	406	23	AAV52206	Human coagulation
41	156	81.7	406	23	AAV52207	Human coagulation
42	156	81.7	406	23	AAV52208	Human coagulation
43	156	81.7	406	23	AAV52209	Human coagulation
44	156	81.7	406	23	AAV52210	Human coagulation
45	156	81.7	406	23	AAV52211	Human coagulation

ALIGNMENTS

RESULT 1	
AAV18312	
ID	AAV18312 standard; peptide; 44 AA.
AC	AAV18312;
XX	
DT	17-AUG-1999 (first entry)
XX	
DE	Modified GIA domain of vitamin K-dependent protein.
XX	
KW	GIA domain; muten; vitamin K-dependent protein; clotting disorder;
XX	
OS	Therapy.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
FT	Key
FT	Misc-difference 1..44
FT	Location/Qualifiers
FT	/note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	
PN	WO9920767-A1.
XX	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98WO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MIND) UNIV MINNESOTA.
XX	
PI	Nelaeuten GL;
XX	

DR WPI; 1999-288309/24.
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 80; 86bp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 Query Match 86.4%; Score 165; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 1.6e-20;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44
 RESULT 2
 AAY18310
 ID AAY18310 standard; peptide; 44 AA.
 AC AAY18310;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 XX
 XX WO9920767-A1.
 XX
 XX 29-APR-1999.
 XX
 XX 20-OCT-1998; 98WO-US22152.
 XX
 XX 23-OCT-1997; 97US-0955636.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX
 XX Nelsestuen GL;
 PI
 DR WPI; 1999-288309/24.
 DR
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 80; 86bp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 Query Match 83.2%; Score 159; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 1.7e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44
 RESULT 3
 AAY18302
 ID AAY18302 standard; peptide; 44 AA.
 AC AAY18302;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 XX
 XX WO9920767-A1.
 XX
 XX 29-APR-1999.
 XX
 XX 20-OCT-1998; 98WO-US22152.
 XX
 XX 23-OCT-1997; 97US-0955636.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX
 XX Nelsestuen GL;
 PI
 DR WPI; 1999-288309/24.
 DR
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Claim 11; Page 81; 86bp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 Query Match 82.7%; Score 158; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2.5e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFDAXRTKLFWISY 44

```

RESULT 4
AA18311
ID AA18311 standard; peptide; 44 AA.
AC AA18311;
XX
XX 17-AUG-1999 (first entry)
XX
XX Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; murein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 1..44
XX /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX MO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;
XX
XX Query Match 82.2%; Score 157; DB 20; Length 44;
XX Best Local Similarity 95.5%; Pred. No. 3.6e-19;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ANAFLXLRQGSILXKXCKXQCSFXXAFIFKDAKRTKLFWISY 44
XX ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX 1 ANAFLXLRQGSILXKXCKXQCSFXXAFIFKDAKRTKLFWISY 44
XX
XX RESULT 5
XX AA18305
XX ID AA18305 standard; peptide; 44 AA.
XX
XX AA18305;
XX
XX 17-AUG-1999 (first entry)
XX
XX Human factor VII GLA domain.
XX
XX GLA domain; vitamin K-dependent protein; clotting disorder;
XX therapy.

```

```

XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX MISC-difference 1..44
XX /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX MO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;
XX
XX Query Match 81.7%; Score 156; DB 20; Length 44;
XX Best Local Similarity 95.5%; Pred. No. 5.4e-19;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ANAFLXLRQGSILXKXCKXQCSFXXAFIFKDAKRTKLFWISY 44
XX ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX 1 ANAFLXLRQGSILXKXCKXQCSFXXAFIFKDAKRTKLFWISY 44
XX
XX RESULT 6
XX AAB36395
XX ID AAB36395 standard; peptide; 44 AA.
XX
XX AAB36395;
XX
XX 27-FEB-2001 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid domain SPQ ID NO:3.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Homo sapiens.
XX
XX WO20006753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.

```

XX (MINU) UNIV MINNESOTA.
 PA NeIsescu GL;
 PI WPI; 2001-007226/01.
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX Disclosure; Page 12; 81pp; English.
 PS The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 CC
 XX Sequence 44 AA:

Query Match 81.7%; Score 156; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 5.4e-19;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLXRCCKXCSCFFXAERIFPDARTKLFWISY 44
 Db 1 ANAFLLXLRQSLXRCCKXCSCFFXAERIFPDARTKLFWISY 44

RESULT 7
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.
 AC AAB84870;
 XX 31-JUL-2001 (first entry)
 DT
 XX Mutant blood coagulant factor VII (FVII-31).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX JP2001061479-A.
 PN 13-MAR-2001.
 PD 24-AUG-1999; 99JP-0237610.
 PF 24-AUG-1999; 99JP-0237610.
 PR 24-AUG-1999; 99JP-0237610.
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX Claim 14; Page 20-21; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX
 XX Sequence 401 AA;

Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 5.1e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLXRCCKXCSCFFXAERIFPDARTKLFWISY 44
 Db 1 ANAFLELRPSGLRCKEBCSCFEAREIFPDARTKLFWISY 44

RESULT 8
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.
 AC AAB84871;
 XX 31-JUL-2001 (first entry)
 DT
 XX Mutant blood coagulant factor VII (FVII-39).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 FT Asp-Arg-Lys-Thr-Leu"
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX JP2001061479-A.
 PN 13-MAR-2001.
 PD 24-AUG-1999; 99JP-0237610.
 PF 24-AUG-1999; 99JP-0237610.
 PR 24-AUG-1999; 99JP-0237610.
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX Claim 16; Page 23-24; 29pp; Japanese.
 PS The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX
 XX Sequence 401 AA;

Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 5.1e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Query Match	Best Local Similarity	81.7%	Score 156;	DB 18;	Length 406;
Matches 32;	Conservative	72.7%;	Pred. No. 5.1e-18;	Mismatches 12;	Indels 0;
					Gaps 0;
FT	Disulfide-bond	91..102			
FT	Disulfide-bond	98..112			
FT	Disulfide-bond	114..127			
FT	Disulfide-bond	135..162			
FT	Cleavage-site	143..144			
FT	Modified-site	145			
FT	/note= "proteolytic site"				
FT	Disulfide-bond	159..164			
FT	Disulfide-bond	178..194			
FT	Active-site	193			
FT	Active-site	242			
FT	Active-site	344			
FT	Cleavage-site	290..291			
FT	/note= "proteolytic site in unmodified factor VII"				
FT	Misc-difference	290			
FT	/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"				
FT	Disulfide-bond	310..329			
FT	Cleavage-site	315..316			
FT	/note= "proteolytic site"				
FT	Modified-site	322			
FT	/note= "glycosylation site"				
FT	Disulfide-bond	340..368			
FT	Cleavage-site	341..342			
FT	/note= "proteolytic site"				
FT	Cleavage-site	392..393			
FT	/note= "proteolytic site"				
FT	Cleavage-site	396..397			
FT	/note= "proteolytic site"				
FT	Cleavage-site	402..403			
FT	/note= "proteolytic site"				
XX					
PN	US5580560-A.				
XX					
PD	03-DEC-1996.				
XX					
PP	13-NOV-1989;	89US-0434149.			
XX					
PR	09-AUG-1993;	93US-0104509.			
PR	13-NOV-1989;	89US-0434149.			
PR	12-JUN-1992;	92US-0898248.			
PR	22-AUG-1994;	94US-0293778.			
XX					
PA	(NOVO) NOVO-NORDISK AS.				
XX					
PI	Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;				
XX					
DR	WPI; 1997-033523/03.				
XX					
FT	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability				
XX					
PS	Example 3; Page -; 28pp; English.				
XX					
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg280, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein.				
CC					
XX					
SQ	Sequence 406 AA;				

[illegible]


```

FT FT Modified-site 145 /note= "glycosylation site"
FT FT Disulfide-bond 159..164
FT FT Disulfide-bond 178..194
FT FT Active-site 193
FT FT Active-site 242
FT FT Active-site 344
FT FT Cleavage-site 290..291
FT FT /note= "proteolytic site"
FT FT Disulfide-bond 310..329
FT FT Cleavage-site 315..316
FT FT /note= "proteolytic site in unmodified factor VII"
FT FT Misc-difference 315 /note= "native Arg315 has been substituted by Ser to
FT FT provide a proteolytically more stable peptide
FT FT bond"
FT FT Modified-site 322 /note= "glycosylation site"
FT FT Disulfide-bond 340..368
FT FT Cleavage-site 341..342
FT FT /note= "proteolytic site"
FT FT Cleavage-site 392..393
FT FT /note= "proteolytic site"
FT FT Cleavage-site 396..397
FT FT /note= "proteolytic site"
FT FT Cleavage-site 402..403
FT FT /note= "proteolytic site"
XX PN USS580560-A.
XX XX
XX PD 03-DEC-1996.
XX PF 13-NOV-1989; 89US-0434149.
XX PR 09-AUG-1993; 93US-0104509.
XX PR 13-NOV-1989; 89US-0434149.
XX PR 12-JUN-1992; 92US-0896248.
XX PR 22-AUG-1994; 94US-0293778.
XX PA (NOVO ) NOVO-NORDISK AS.
XX XX
XX PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX DR WP1; 1997-033523/03.
XX XX
XX PT Mutated human factor VII or VIIa proteins - with amino acid
XX PT substitutions to improve proteolytic stability
XX PS Example 4; Page -: 28pp; English.
XX XX
XX CC Modified human factor VII or VIIa proteins are stabilised against
XX CC proteolytic cleavage by substitution of one of the residues Lys32,
XX CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX CC Lys341 by an amino acid that provides a proteolytically more stable
XX CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX CC bleeding disorders such as thrombocytopenia and von Willebrand's
XX CC disease. They are also suitable for addition to plasma substitutes.
XX CC The present sequence is a specific example of a modified factor VII
XX CC protein.
XX CC
XX SO Sequence 406 AA;
OY Query Match 81.7%; Score 156; DB 18; Length 406;
OY Best Local Similarity 72.7%; Pred. No. 5,1e-18;
OY Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0.
Db 1 ANAFLXLRQGLRXCKXXCSPXXAFXPDPDAXRTKLFWISY 44
1 ||||| ||||| ||||| ||||| |||||
1 ANAFLELRPGSLERCKEKCQCSFEARKEIFKDAERTKLFWISY 44

```

```

AUU77745
ID AUU77745 standard; protein, 406 AA.
XX AC AUU77745;
XX DT 05-JUN-2002 (first entry)
XX DE Human factor VIIa active site mutant.
XX KM Factor VIIa; human; shock heat treatment; protein stability;
OS protein manufacture; protein conformation; mutant, mutein.
XX OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT Active-site 193 /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242 /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344 /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344 /label= Gly, Met, Thr
FT /note= "Preferably Ala, wild type Ser"
FT WO200177141-A1.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-DK00234.
XX PR 06-APR-2000; 2000DK-0000573.
XX PR 17-APR-2000; 2000US-197650P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Mathiesen F;
XX DR WPI; 2001-657162/75.
XX PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX PT involves a shock heat treatment -
XX PS Disclosure; Page -: 22pp; English.
XX CC The invention describes a method of stabilising a polypeptide involving
CC shock heat treatment of the polypeptide. The method is useful in a
CC pharmaceutical composition, in the industrial or large scale method of
CC manufacturing a polypeptide, also as a unit operation during preparation,
CC purification, recovery and/or formulation of polypeptides. The shock heat
CC treatment improves the protein stability without substantial loss of
CC biological activity. The method can be applied to change polypeptide
CC conformation in a very fast and non-invasive manner. The polypeptide
CC formed is stable. The method is also useful for decreasing the
CC association of the polypeptide. This sequence represents a modified
CC human factor VIIa protein, mutated at the catalytic site, described
CC in the invention.
CC Note: This sequence does not appear in the specification but has
CC been obtained using information given in the invention.
SQ Sequence 406 AA;

Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 5,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0.

1 ANAFLXLRLRGSLRXCKXKOCSPFXAFIFPDAXRTKLFWISY 44
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ANAFLLELRPGSLRECKEBOCSFEARATIFDARTKLFWISY 44

```



```

PR 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
PI Andersen KV, Pedersen AH, Bornaes C;
XX
DR WPI; 2001-581807/65.
DR N-PSDB; AA199983.
XX
PT New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX
PS Disclosure; Page 85-86; 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased bioavailability in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
CC
XX
SQ Sequence 406 AA;
XX
Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 5,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Cy 1 ANAFPLXLRQGSIXRCKXKOCSEFXAFIFPDARXTLFWISY 44
Db 1 ANAFLELRPGSLERECKECCFEAREIFPDARTKLFWISY 44
RESULT 15
AAM52181
ID AAM52181 standard; Procein; 406 AA.
XX
XX AAM52181;
XX
AC AAM52181;
XX
DT 07-FEB-2002 (first entry)
XX
DB Human FVII mutant T106N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW mutcin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 14 /note= "OTHER = gamma carboxylutamic acid"
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 16 /label= Glu, OTHER
FT /label= Glu, OTHER

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FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT
FT Modified-site 52 /note= "OTHER = gamma carboxylutamic acid"
FT
FT Modified-site 60 /note= "O-glycosylated"
FT
FT Misc-difference 106 /note= "O-glycosylated"
FT
FT Modified-site 145 /note= "wild-type Thr substituted by Asn"
FT
FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT
FT Modified-site 322 /note= "N-glycosylated"
FT
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK0094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
PI Andersen KV, Pedersen AH, Bornaes C;
XX
XX
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -: 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased bioavailability in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.

```

CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).

XX
SQ Sequence 406 AA;

Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 5.1e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKXXQCSFXXAFXIFKDXRRKLFWISY 44
|||
DB 1 ANAFLLXLRPGSLRXCKXXQCSFXXARXIFKDXRRKLFWISY 44

Search completed: March 19, 2003, 14:51:09
Job time : 31.4375 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLN28PHE

Perfect score: 191

Sequence: 1 ANMFLXLRGSLRXCKXX.....XXAFXIFKDXRTFLFWISY 44

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	1 KFHU7	coagulation factor
2	122	63.9	443	2 I46932	coagulation factor
3	114	59.7	407	1 KPB07	coagulation factor
4	99	51.8	492	1 EXBO	coagulation factor
5	97	50.8	461	1 UX0210	protein C (activat
6	96	50.3	461	1 S18994	protein C (activat
7	96	50.3	461	1 EXHU	coagulation factor
8	94	49.2	622	1 THHU	thrombin (EC 3.4.2
9	90	47.1	482	1 EXRT	coagulation factor
10	90	47.1	617	2 S10511	thrombin (EC 3.4.2
11	90	47.1	478	2 A35827	thrombin (EC 3.4.2
12	89	46.6	475	1 EXCH	coagulation factor
13	88	46.1	456	1 KXBO	coagulation factor
14	81	42.4	461	1 KKHU	protein C (activat
15	80	41.9	461	1 KKHU	coagulation factor
16	79	41.4	416	1 KPB0	coagulation factor
17	74	38.7	625	1 TBBO	thrombin (EC 3.4.2
18	71	37.2	452	1 A30351	coagulation factor
19	71	37.2	459	2 U00419	coagulation factor
20	67	35.1	642	2 S53433	plasma protein S p
21	62	32.5	642	2 S53434	plasma protein S p
22	62	32.5	676	1 KKHUS	plasma protein S p
23	60	31.4	675	1 KXBOS	plasma protein S p
24	58	30.4	396	1 KXBOS	plasma protein S p
25	58	30.4	646	2 S38819	plasma protein S -
26	57	29.8	676	1 KXRTS	plasma protein S p
27	55.5	29.1	575	2 G96763	probable MAP kinase
28	53	27.7	422	1 KKHUZ	plasma protein Z p
29	53	27.7	673	2 A48089	growth arrest-spec

30	51	26.7	674	2 I55476	growth potentiating
31	51	26.7	678	1 B48089	growth arrest-spec
32	50	26.2	675	2 KXMS	plasma protein S p
33	49.5	25.9	594	2 D84859	probable MAP kinase
34	49.5	25.9	603	2 C96575	probable MAP kinase
35	47.5	24.9	271	2 S66591	probable membrane
36	45.5	23.8	83	2 T17839	hypothetical prote
37	45	23.6	52	2 T19574	hypothetical prote
38	45	23.6	879	2 S55864	hypothetical prote
39	45	23.6	907	2 T15792	hypothetical prote
40	44	23.0	306	2 I49068	protein kinase STY
41	43	22.5	394	1 S30286	tetracycline resist
42	43	22.5	440	2 C70198	conserved hypothe
43	42	22.0	486	2 T06770	cellulase (EC 3.2.
44	42	22.0	1559	2 T07757	probable DNA (cyto
45	41.5	21.7	161	2 F82637	conserved hypothe

ALIGNMENTS

RESULT 1

coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000

C:Accession: A28322; A28819; A31186; B31186; S63524

R:O'Hara, P.J.; Grant, F.J.; Haldean, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murte

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend

A:Reference number: A28322; MUID:87260948; PMID:3037537

A:Accession: A28322

A:Molecule type: DNA

A:Residues: 1-466 <OHA>

A:Cross-references: GB:U02933; NID:G180333; PIDN:AAA51983.1; PID:G180334

R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A:Title: Characterization of a cDNA coding for human factor VII.

A:Reference number: A28819; MUID:86205965; PMID:3486420

A:Accession: A28819

A:Molecule type: mRNA

A:Residues: 1-466 <HAG>

A:Cross-references: GB:M13232; NID:G182799; PIDN:AAA8040.1; PID:G182801

R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.;

Biochemistry 27, 7785-7793, 1988

A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr

A:Reference number: A90539; MUID:89088153; PMID:3264725

A:Accession: A31186

A:Molecule type: protein

A:Residues: 61-212 <THI>

A:Accession: B31186

A:Molecule type: protein

A:Residues: 213-466 <TH2>

R:Bjorn, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A:Reference number: A40529; MUID:91250411; PMID:1904059

A:Contents: annotation; and posttranslational modifications of human factor VII-a fr

R:Persson, E.; Petersen, L.C.

Eur. J. Biochem. 234, 293-300, 1995

A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A:Reference number: S63524; MUID:96096752; PMID:8529655

A:Accession: S63524

A:Molecule type: protein

A:Residues: 61-65;99-103;105-109;213-217;308-312 <BER>

C:Genetics:

A:Gene: GDB:F7

A:Cross-references: GDB:119897; OMIM:227500

A:Map position: 13q34-13q34

A:Insertion: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C:Function: A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser

coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-20/Domain: signal sequence #status predicted <PRO>
 F:21-60/Domain: propeptide #status predicted <PRO>
 F:61-104/Domain: Gla domain homology <GLA>
 F:161-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:110-140/Domain: EGF homology <EG1>
 F:151-187/Domain: EGF homology <EG2>
 F:213-444/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:213-444/Domain: trypsin homology <TRY>
 F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
 F:112/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
 F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:212-213/Cleavage site: Arg-Ile (coagulation factor XIIIa) #status experimental
 F:253,302,404/Active site: His, Asp, Ser #status predicted
 F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.7%; Score 156; DB 1; Length 466;
 Best Local Similarity 72.7%; Pred. No. 7, 6e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKKXQCSFXXAFIKDAXRTKLFWISY 44
 DB 61 ANAFLEELRPGSLRCKECCQCFEFAREIFKDAERTKLFWISY 104

RESULT 2
 146932
 coagulation factor VII - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C:Accession: 146932
 R:Brothers, A.B.; Clarke, B.D.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A:Reference number: 146932; MUID:93190306; PMID:8383565
 A:Accession: 146932
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <BRO>
 A:Cross-references: GB:S56300; NID:9266294; PID:9266295
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:24-83/Domain: Gla domain homology <GLA>
 F:89-120/Domain: EGF homology <EG1>
 F:130-166/Domain: EGF homology <EG2>
 F:192-425/Domain: trypsin homology <TRY>

Query Match 63.9%; Score 122; DB 2; Length 443;
 Best Local Similarity 54.5%; Pred. No. 5, 2e-13;
 Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKKXQCSFXXAFIKDAXRTKLFWISY 44
 DB 40 ANSFLEELRPGSLRCKECCQCFEFAREVFQSTERTKQFWISY 83

RESULT 3
 KFB07
 coagulation factor VIIa (BC 3.4.21.21) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
 C:Accession: A31979; C20274
 R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamachi, Y.; Miyata, T.; Iwanaga, S.
 J. Biol. Chem. 263, 14868-14877, 1988
 A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
 A:Reference number: A31979; MUID:89008362; PMID:3049594
 A:Accession: A31979
 A:Molecule type: protein
 A:Contents: annotation; revision to residue 103
 A:Title: Bovine factor X-1 (Stuart factor); amino-acid sequence of heavy chain.
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor
 A:Reference number: A20274; MUID:83308613; PMID:6688526
 A:Accession: C20274
 A:Molecule type: protein
 A:Residues: 58-62, 'X', 64-68 <MCN>
 A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
 J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX
 A:Reference number: A44556; MUID:8921999; PMID:3149637
 A:Contents: annotation
 A:Note: structure and location of covalently bound carbohydrate
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:1-44/Domain: Gla domain homology (fragment) <GLA>
 F:50-81/Domain: EGF homology <EG1>
 F:91-127/Domain: EGF homology <EG2>
 F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:153-387/Domain: trypsin homology <TRY>
 F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/
 F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:152-153/Cleavage site: Arg-Ile (coagulation factor XIIIa) #status experimental
 F:193,242,344/Active site: His, Asp, Ser #status predicted
 F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 59.7%; Score 114; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 1, 1e-11;
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKKXQCSFXXAFIKDAXRTKLFWISY 44
 DB 1 ANGFLEELRPGSLRCKECCQCFEFAREIFRNERTRQFWISY 44

RESULT 4
 EXBO
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine
 N:Alternate names: Stuart factor
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
 R:Fung, W.R.; Campbell, R.M.; MacGillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A:Reference number: A22867; MUID:84247315; PMID:6330671
 A:Accession: A22867
 A:Molecule type: mRNA
 A:Residues: 1-487 <ENF>
 A:Cross-references: GB:X00673; NID:9192; PID:CAA25286.1; PID:9193
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titeni, K.
 Biochemistry 19, 659-667, 1980
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A:Reference number: A14997; MUID:80130563; PMID:6766735
 A:Accession: A14997
 A:Molecule type: protein
 A:Residues: 41-102, 'N', 104-180 <ENF>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor X-1 (Stuart factor)
 A:Reference number: A20274; MUID:83308613; PMID:6688526
 A:Contents: annotation; revision to residue 103
 A:Title: Bovine factor X-1 (Stuart factor); amino-acid sequence of heavy chain.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A:Title: Bovine factor X-1 (Stuart factor); amino-acid sequence of heavy chain.

F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.3%; Score 96; DB 1; Length 488;

Best Local Similarity 38.6%; Pred. No. 1,7e-08;

Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

1 ANAFXXLRGSLKRXCKXCFXAFKIFKDXRTLFWISY 44

41 ANSFLBKKKGLHREKMEETCSYEAREVEDSDKTNEFWNKY 84

RESULT 8

Thrombin (EC 3.4.21.5) precursor [validated] - human

N:Alternate names: coagulation factor II

N:Contains: prothrombin

C:Species: Homo sapiens (man)

C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000

C:Accession: A29351; A00914; B00914; A37549; A37550; I51952

R:Degen, S.J.F.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A:Title: Nucleotide sequence of the gene for human prothrombin.

A:Reference number: A29351; PMID:8807877; PMID:2825773

A:Accession: A29351

A:Molecule type: DNA

A:Residues: 1-622 <DEG>

A:Cross-references: GB:M17262; GB:M3691; NID:G558069; PIDN:AA63054.1; PID:G339641

A:Accession: B00914

A:Molecule type: DNA

A:Residues: 188-311 <DE3>

R:Malz, D.A.; Hewitt-Emmett, D.; Seegers, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977

A:Reference number: A37549; PMID:77193964; PMID:266717

A:Accession: A37549

A:Molecule type: protein

A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,

R:Butkowski, R.J.; Eliott, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.

A:Reference number: A37550; PMID:77207112; PMID:873923

A:Accession: A37550

A:Molecule type: protein

A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-

R:Rahier, M.J.; Blashill, A.; Furtle, B.; Furtle, B.C.

J. Biol. Chem. 261, 13210-13215, 1986

A:Reference number: A37551; PMID:87008532; PMID:3759958

A:Accession: A37551

C:Genetics:
A:Gene: GDB:F2
A:Cross-references: GDB:119894; OMIM:176930

A:Map position: 11p11-11q12

A:Insertions: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/

C:Superfamily: thrombin; Gla domain homology; Kringle homology; trypsin homology

C:Keywords: acute phase; blood coagulation; calcium binding; carboxylutamic acid; duplic

F:124/Domain: signal sequence #status predicted <SIG>

F:25-43/Domain: propeptide #status predicted <PRO>

F:28-87/Domain: Gla domain homology <Gla>

F:44-622/Product: prothrombin #status experimental <MAT>

F:44-327/Domain: activation peptide #status experimental <APT>

F:213-291/Domain: kringle homology <KR1>

F:328-363/Product: thrombin light chain #status experimental <LCH>

F:364-622/Product: thrombin heavy chain #status experimental <HCH>

F:364-613/Domain: trypsin homology <TRY>

F:49,50,57,62,63,68,69,72,75/Modified site: gamma-carboxylutamic acid (Glu) #status

F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Dissulfide bonds: #status

F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted

F:336-482,536-550,564-594/Dissulfide bonds: #status predicted

F:331-407/Dissulfide bonds: #status experimental

F:406,462/Active site: His, Asp #status predicted

F:416/Binding site: carboxylate (Asn) (covalent) #status experimental

F:568/Active site: Ser #status experimental

Query Match 49.2%; Score 94; DB 1; Length 622;

Best Local Similarity 38.6%; Pred. No. 4.6e-06;

Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

1 ANAFXXLRGSLKRXCKXCFXAFKIFKDXRTLFWISY 44

44 ANSFLBKKKGLHREKMEETCSYEAREVEDSDKTNEFWNKY 87

RESULT 9

EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text change 08-Dec-2000

C:Accession: S49075; JC4670; PS0191; PS0190; 162745

R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Thromb. Res. 80, 63-73, 1995

A:Title: Evidence for competition between vitamin K-dependent clotting factors for intrac

A:Reference number: A58498; PMID:96093366; PMID:8578539

A:Accession: S49075

A:Molecule type: mRNA

A:Residues: 1-482 <STRA2>

A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601

C:Accession: S15838; S20380; S20381
R:Shukri, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:CROSS-references: DDBJ: D00844; NID:9222869; PIDN:BA00724.1; PID:9222870
R:Goton, B.; Yamachi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsi
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <G02>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-40/Domain: propeptide #status predicted <PRO>
F:23-84/Domain: Gla domain homology <GUA>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <AP>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <ANC>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #
F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:186,207,228,285/Binding site: carboxylate (Asn) (covalent) #status predicted
F:28,338,425/Active site: His, Asp, Ser #status predicted

Query Match 46.6%; Score 89; DB 1; Length 475;
Best Local Similarity 38.6%; Pred. No. 2.6e-07;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLXLRQSLKRXCKXQCSFXXAFIFDAXRTLFWISY 44
Db 41 ANSFLEMKQGNIRECNBERCSKEAREAPFEDNKTETEFWNY 84

RESULT 13
KXBO
protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence revision 17-Mar-1997 #text_change 16-Jul-1999
C:Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826; PMID:6091100
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <L0N>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6896876
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <FER>
A>Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: Beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326; PMID:6896877
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV' <STB>
R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless pr
A:Reference number: A37541; MUID:83213513; PMID:6304092
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+ bind
A:Reference number: A37542; MUID:83213514; PMID:6406503
A:Contents: annotation; activation; calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg
B.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is cl
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stron
Cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding,
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GUA>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Product: EGF homology <EG1>
F:137-122/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <AP>
F:211-440/Domain: trypsin homology <TRY>
F:45,46,53,55,58,59,62,64,65,66,74/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #statu
F:136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 46.1%; Score 88; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 3.8e-07;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANAFLXLRQSLKRXCKXQCSFXXAFIFDAXRTLFWISY 44
Db 40 ANSFLELRPGNVERECSEVCEFEAREIFONTEDTAFWSFY 83

RESULT 14
KXHU
protein C (activated) (EC 3.4.21.69) precursor - human
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22331; A25426; A21781; A23789; A00927
R:Forster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A:Title: The nucleotide sequence of the gene for human protein C.
A:Reference number: A22331; MUID:85270390; PMID:2991887
A:Accession: A22331
A:Molecule type: DNA
A:Residues: 1-461 <F0S1>
A:CROSS-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A:Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471
A:Accession: A25426
A:Molecule type: DNA
A:Residues: 1-445, 'L', 446-461 <PU>
A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
R:Poster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A:Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781; MUID:84272714; PMID:6589623
A:Accession: A21781
A:Molecule type: mRNA
A:Residues: 'Q', 107-461 <POS>
A:Cross-references: GB:X02059; NID:9190322; PIDN:AAA60164.1; PID:9190323
R:Beckmann, R.J.; Schmidt, R.J.; Satterre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and
A:Reference number: A23789; MUID:85269639; PMID:2991859
A:Accession: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
R:Milietich, J.P.; Broze Jr., G.U.
J. Biol. Chem. 265, 11397-11404, 1990
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation
A:Reference number: A44605; MUID:90293094; PMID:1694179
A:Accession: A44605
A:Contents: annotation; carbohydrate binding sites; activation peptide
A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R:Harrie, R.J.; Ling, V.T.; Speltman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor
A:Reference number: A44606; MUID:92184750; PMID:1544894
A:Accession: A44606
A:Contents: annotation; beta-hydroxyaspartic acid
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
activation of factor Va is strongly enhanced by complexing with protein S. Protein C also
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C:Genetics:
A:Gene: GDB:PROC
A:Cross-references: GDB:120317; OMIM:176860
A:Map position: 2q13-2q21
A:Introns: 24/1, 79/3, 88/1, 134/1, 179/1, 226/3, 266/1
A:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-32/Domain: signal sequence #status predicted <SIS>
F:27-86/Domain: Gla domain homology <GUA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-197/Product: protein C light chain #status predicted <LCH>
F:92-131/Domain: EGF homology <EG1>
F:140-175/Domain: EGF homology <EG2>
F:200-461/Product: protein C heavy chain #status predicted <HC>
F:200-211/Domain: activation peptide #status experimental <APT>
F:212-445/Domain: trypsin homology <TRY>
F:48-49, 56-61, 62-67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
F:59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-218, 238-254, 373-387, 398-426/D
F:106-111/disulfide bonds: #status predicted
F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
F:113/Modified site: eythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:139, 290, 335/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
F:253, 299, 402/Active site: His, Asp, Ser #status predicted
F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 42.4%; Score 81; DB 1; Length 461;
Best Local Similarity 43.9%; Pred. No. 6, 1e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLRXKCKXXQGFXXAFKFXRTKLFM 41
DB 43 ANSFLERHSHSLRECEIBICDFEAKKEIFQVNDTLAFW 83

RESULT 15
KFHU

coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N:Alternate names: antihemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence_revision 30-Jun-1987 #text_change 15-Sep-2000
A:Accession: A00922; A37570; A30511; A32989; A26673; A21337; A37546; A30623; A60486; A20
R:Yochitake, S.; Schach, S.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A:Reference number: A00922; MUID:8600558; PMID:29947716
A:Accession: A00922
A:Molecule type: DNA
A:Residues: 1-461 <POS>
A:Cross-references: GB:X02402; NID:9182612; PIDN:AAA59620.1; PID:9182613
R:Ranson, D.S.; Choo, K.H.; Ree, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro
EMBO J. 3, 1053-1060, 1984
A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; MUID:84236100; PMID:6329734
A:Accession: A37570
A:Molecule type: DNA
A:Residues: 1-461 <ANS>
A:Cross-references: GB:X02048
R:Reitman, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
A:Reference number: A30511; MUID:88327116; PMID:3416069
A:Accession: A30511
A:Molecule type: DNA
A:Residues: 8-24 <REL>
A:Cross-references: ENBL:X55008; NID:9311288; PIDN:CAB38245.2; PID:94469253
R:Kobert, D.D.; Bottema, C.D.K.; Buerschede, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
A:Reference number: A32989; MUID:89371752; PMID:2773937
A:Accession: A32989
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOE>
A:Cross-references: GB:X02048
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A26673; MUID:85190593; PMID:3857619
A:Accession: A26673
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <WCG>
A:Cross-references: GB:M11309; NID:9180552; PIDN:AAA52023.1; PID:9180553
A>Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jaye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstosh
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; MUID:83220788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <NAV>
A:Cross-references: GB:J00137; NID:9182610; PIDN:AAA52763.1; PID:9182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M35672
R:Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
A:Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609
A:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990

A>Title: Development of an immunoaffinity process for factor IX purification.
 A/Reference number: A60486; MUID:90194857; PMID:2316207
 A/Accession: A60486
 A/Molecule type: protein
 A/Residues: 47-52,'XX',55-60,'X',62,'XX',65 <THA>
 R/McMullen, B.A.; Fujikawa, K.; Kistel, W.
 A/Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX.
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Accession: A20274
 A/Molecule type: protein
 A/Residues: 105-109,'X',111-115 <MCW>
 R,Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Uirich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A>Title: Characterisation of two differently processed forms of human recombinant factor IX.
 A/Reference number: S02527; MUID:88166735; PMID:3280312
 A/Accession: S02527
 A/Molecule type: protein
 A/Residues: 29-63 <BAL>
 A/Note: processed forms expressed in recombinant system
 R,Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meullen,
 EMBO J. 9, 3295-3301, 1990
 A>Title: Characterization of recombinant human Factor IX expressed in transgenic mice and in transgenic rats.
 A/Reference number: S12058; MUID:9106024; PMID:2209546
 A/Accession: S12058
 A/Molecule type: protein
 A/Residues: 1-68 <JAL>
 A/Note: processed forms expressed in recombinant system
 R,Hanford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium binding site.
 A/Reference number: S12377; MUID:90151623; PMID:2406129
 A/Accession: S12377
 A/Molecule type: protein
 A/Residues: 92-130 <HAN>
 A/Note: NMR detection of calcium binding by domain expressed in recombinant system
 R,de la Sall, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A/Reference number: I59612; MUID:94054330; PMID:8236150
 A/Accession: I59612
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 444-461 <RES>
 A/Cross-references: GB:S66752; NID:9439773; PIDN:AA82888.1; PID:9439774
 R,Stoflet, E.S.; Koebberl, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A>Title: Genomic amplification with transcript sequencing.
 A/Reference number: I59529; MUID:88127096; PMID:3340835
 A/Accession: I59529
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 290-359 <RE2>
 A/Cross-references: GB:M9063; NID:G182622; PIDN:AA52456.1; PID:G182623
 R,Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A>Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
 A/Reference number: A54255; MUID:94227047; PMID:8172892
 A/Accession: A54255
 A/Molecule type: protein
 A/Residues: 'D',204,'X',206-211,212,'D',214,'X',216-221,'D' <AGA>
 A/Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R,Di Sciopio, R.G.; Kuvachl, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A>Title: Activation of human factor IX (Christmas factor).
 A/Reference number: A18483; MUID:78194509; PMID:659613
 A/Contents: annotation; activation; active site; carbohydrate binding
 R,McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A/Reference number: A37569
 A/Contents: annotation
 A/Note: 194-Thr was also found
 R,Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 259, 5698-5704, 1984
 A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site.
 A/Reference number: A37543; MUID:84185715; PMID:6425296
 A/Contents: annotation; calcium binding
 R,Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A/Reference number: A37544
 A/Contents: annotation; calcium binding, correction
 R,Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A/Reference number: A37545; MUID:86189947; PMID:3009023
 A/Contents: annotation; signal sequence cleavage site
 R,Suhiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A>Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
 A/Reference number: A30622; MUID:90078223; PMID:2552373
 A/Contents: annotation; sequence of mutant B(M) Nagoya
 A/Note: carboxylation, glycosylation, and cleavage sites
 R,Barton, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee
 submitted to the Brookhaven Protein Data Bank, November 1991
 A/Reference number: A51252; PDB:1IXA
 A/Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A/Note: recombinant form expressed in yeast
 C/Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
 C/Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 A/Genes: GDB:F9
 A/Cross-references: GDB:119900; OMIM:306900
 A/Map position: Xq27.1-Xq27.2
 A/Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C/Function:
 A>Description: catalyzes the proteolytic activation of coagulation factor X in the presen
 A/Pathway: blood coagulation intrinsic pathway
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutami
 F:1-88/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <Gla>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:134-170/Domain: EGF homology <EGF>
 F:192-226/Domain: EGF homology <EG2>
 F:227-461/Product: activation peptide #status experimental <ACT>
 F:227-454/Domain: trypsin homology <TRY>
 F:53,54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 41.9%; Score 80; DB 1; Length 461;
 Best Local Similarity 42.9%; Pred. No. 9 1e-06;
 Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 10 QGSLRXCKXXQCSFXAFAIFKDAKRTKFWISY 44
 DB 57 QGNLERCEMEKCSFEARVEFEMTERTFEMKQY 91

Search completed: March 19, 2003, 15:00:50
 Job time : 30.125 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLN28PHE
Sequence: 1 ANAFLLXLRQSLXRCCKX.....XXAFYIFKDXKRTYLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 40 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	FA7_HUMAN	P08709 homo sapien
2	122	63.9	444	FA7_RABIT	P98139 oryctolagus
3	114	59.7	407	FA7_BOVIN	P22457 bos taurus
4	111	58.1	446	FA7_MOUSE	P70375 mus musculus
5	102	53.4	490	FA10_RABIT	O19045 oryctolagus
6	98	51.8	492	FA10_BOVIN	P00743 bos taurus
7	98	51.3	459	PRTC_PIG	O99132 sus scrofa
8	97	50.8	218	TMG1_HUMAN	O14668 homo sapien
9	97	50.8	461	PRTC_MOUSE	P13587 mus musculus
10	96	50.3	461	PRTC_RAT	P13394 rattus norv
11	96	50.3	488	FA10_HUMAN	P00742 homo sapien
12	94	49.2	622	THRB_HUMAN	P00734 homo sapien
13	90	47.1	617	THRB_RAT	P18292 rattus norv
14	90	47.1	618	THRB_MOUSE	P19221 mus musculus
15	89	46.6	231	TMG3_HUMAN	O98247 homo sapien
16	89	46.6	475	FA10_CHICK	P23155 gallus galli
17	88	46.1	456	PRTC_BOVIN	P00745 bos taurus
18	81	42.4	458	PRTC_RABIT	O26661 oryctolagus
19	81	42.4	461	PRTC_HUMAN	O4070 homo sapien
20	80	41.9	461	FA9_HUMAN	P00740 homo sapien
21	79	41.4	416	FA9_BOVIN	P00741 bos taurus
22	76	39.8	376	FA10_TROCA	P81428 tropidichis
23	74	38.7	625	THRB_BOVIN	P00735 bos taurus
24	73	38.2	202	TMG2_HUMAN	O14669 homo sapien
25	71	37.2	452	FA9_CANFA	P19540 canis famli
26	71	37.2	459	FA9_MOUSE	P16294 mus musculus
27	66.5	34.8	226	TMG4_HUMAN	O98246 homo sapien
28	62	32.5	649	PRTC_TACMU	O28520 macaca mula
29	62	32.5	676	PRTC_HUMAN	P07225 homo sapien
30	60	31.4	675	PRTC_BOVIN	P00724 bos taurus
31	58	30.4	396	PRTC_BOVIN	P00744 bos taurus
32	58	30.4	646	PRTC_RABIT	P98118 oryctolagus
33	57	29.8	675	PRTC_RAT	P53813 rattus norv

34	53	27.7	400	1	PRTC_HUMAN	P22891 homo sapien
35	50	26.2	675	1	PRTC_MOUSE	O08761 mus musculus
36	47.5	24.9	271	1	MD12_YEAST	O92328 saccharomyc
37	45	23.6	879	1	YN65_YEAST	P42837 saccharomyc
38	43	22.5	394	1	TCR4_SALOR	P33733 salmonella
39	43	22.5	440	1	Y788_BORBU	O51728 borrelia bu
40	41	21.5	263	1	PFLA_STRMU	O68575 streptococc
41	41	21.5	393	1	DPS5_PINSY	O02323 pinus sylve
42	41	21.5	616	1	JEN1_YEAST	P36035 saccharomyc
43	40	20.9	343	1	HMD_METVO	O50840 methanococc
44	40	20.9	353	1	HMD_METTL	O50759 m coenzyme
45	40	20.9	602	1	VE1_CRPVK	P03112 cottoncattai

ALIGNMENTS

RESULT 1
FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709:014339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.;"
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.;"
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.
RX Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RX Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.;"
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wildberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.;"
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [17]
 RP STRUCTURE OF CARBOHYDRATE ON SFR-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598953;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPT mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [110]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=96867502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gipeert G.P., Forzen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [111]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [112]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Denosa V., Pinotti M.,
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [113]
 RP VARIANT TYR-238.
 RX MEDLINE=99372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [114]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembail-Cook G., Marin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [115]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chating S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [161]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [117]
 RP VARIANT MET-HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohwata M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg (247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [118]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [119]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [120]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligson U.;
 RT "A1a24Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [121]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDANT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 81.7%; Score 156; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1,1e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLKRXCKXQCSFXXAFYIFDAXRTKLFWISY 44
Db 61 ANAFLELRPGSLERCKEKEQCSFEARAFIFDAERTKLFWISY 104

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
ID FA7_RABIT
AC P98139; P79224; (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (serum prothrombin conversion accelerator).
DE F7.
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."
RT Thromb. Res. Suppl. 69:231-236(1993).
RL [2]
RN REVISION TO 395.
RP TISSUE=Liver;
RC Ruiz S.R., Blajchman M.A., Clarke B.J.;
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RL -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U77477; AAB37326.1; -.
CC HSSP; P08709; 1FAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00089; trypsin. 1.
DR Pfam; PF00594; gla. 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA. 1.
DR SMART; SM00001; EGF_Like. 1.
DR SMART; SM00069; GLA. 1.
DR SMART; SM00020; Tryp_Spc. 1.
DR PROSITE; PS00010; ASX_HYDROXYL. 1.
DR PROSITE; PS00022; EGF 1. 1.
DR PROSITE; PS01186; EGF 2. 1.
DR PROSITE; PS01187; EGF_CA. 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION. 1.
DR PROSITE; PS50240; TRYPSIN_DOM. 1.
DR PROSITE; PS00134; TRYPSIN_HIS. 1.
DR PROSITE; PS00135; TRYPSIN_SER. 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; signal; Hydroxylation.
KW EGF-like domain; Repeat; signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABCFE5427F8 CMC64;

Query Match 63.9%; Score 122; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 9.7e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLKRXCKXQCSFXXAFYIFDAXRTKLFWISY 44
Db 40 ANAFLELRPGSLERCKEKEQCSFEARAFIFDAERTKLFWISY 83

RESULT 3

FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.
OC NCBI_Taxid=9913;
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimomichi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RT J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=9134709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RL
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR PIR: A31979; A31979.
DR HSSP: P08709; 1BP9.
DR MEROPS: S01.215;
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001438; EGF-II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF 2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFblood.
DR PRINTS: PR00001; GLABlood.
DR SMART: SM00179; EGF CA; 1.
DR SMART: SM00001; EGF_like; 1.

DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_spec; 1.
DR PROSITE: PS00010; Asx_hydroxyl; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF 2; 2.
DR PROSITE: PS01187; EGF CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT DOMAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 GLA-RICH.
FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 87 128 EGF-LIKE 2.
FT DOMAIN 153 407 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR THROMBIN).
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLCNAc . . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAc . . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAc . . .).
SQ SEQUENCE 407 AA, 44431 MW, 703E1FE0636F7F10 CRC64;
Query Match 59.7%; Score 114; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 2,3e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
QY 1 ANAFLLKRGSLAKKCKXGCSFXAARFIPDARTKTFWISY 44
DB 1 ANGFLLELLPSLIERCRELCSFEBAHIFRNEERTROFWISY 44
RESULT 4
FA7_MOUSE STANDARD; PRT; 446 AA.
ID FA7_MOUSE
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@sdb.ch).
 CC -----
 CC EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BF9.
 DR MEROPS; S01.215; -.
 DR MCD; MGI.109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS001187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Blood coagulation; zymogen; glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT CHAIN 194 446
 FT DOMAIN 47 76
 FT DOMAIN 87 123

FT DOMAIN 128 169
 FT DOMAIN 194 446
 FT SITE 193 194
 FT
 FT ACT_SITE 234 234
 FT ACT_SITE 283 283
 FT ACT_SITE 385 385
 FT BINDING 379 379
 FT DISULFID 58 63
 FT DISULFID 91 102
 FT DISULFID 96 111
 FT DISULFID 113 122
 FT DISULFID 132 143
 FT DISULFID 139 153
 FT DISULFID 155 168
 FT DISULFID 176 303
 FT DISULFID 200 205
 FT DISULFID 219 235
 FT DISULFID 351 370
 FT DISULFID 381 409
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 76 76
 FT MOD_RES 104 104
 FT CARBOHYD 186 186
 FT CARBOHYD 244 244
 FT SEQUENCE 446 AA; 50276 MW; 2512E4A45C96E CRC64;
 Query Match 58.1%; Score 111; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 8.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
 Oy 1 ANAFLLXLRQGSILKRXCKXKOCSPFXAXFYIKDAXRTLFMISY 44
 Db 42 ANSLLEELWPGSLRECEBQCSFEAREIFKSPERTQFMIVY 85
 RESULT 5
 FA10_RABIT STANDARD; PRT; 490 AA.
 AC OL9045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X.";
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM (BY SIMILARITY).
 CC -1- PM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF003200; AAB62542.1; -.
 CC HSSP: P00742; IHCG.
 DR MEROPS: S01.216; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYD_SPC; 1.
 DR PROSITE: PS00010; ASK_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_Ser; 1.
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat.
 FT SIGNAL 1 20
 FT PROPEP 21 40
 FT CHAIN 41 180
 FT CHAIN 184 490
 FT PROPEP 184 232
 FT CHAIN 233 490
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 233 490
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66

FT MOD_RES 69 69
 FT MOD_RES 72 72
 FT MOD_RES 75 75
 FT MOD_RES 79 79
 FT MOD_RES 103 103
 FT ACT_SITE 274 274
 FT ACT_SITE 320 320
 FT ACT_SITE 417 417
 FT DISULFID 95 101
 FT DISULFID 112 121
 FT DISULFID 129 140
 FT DISULFID 136 149
 FT DISULFID 151 164
 FT DISULFID 172 340
 FT DISULFID 229 244
 FT DISULFID 259 275
 FT DISULFID 388 402
 FT DISULFID 413 441
 FT CARBOHYD 61 61
 FT CARBOHYD 187 187
 FT CARBOHYD 205 205
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;
 Query Match 53.4%; Score 102; DB 1; Length 490;
 Best Local Similarity 40.9%; Pred. No. 3.4e-10;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ANAFELXLRQGLXKXCKXQCSFXXAFIFDKARTKLFATSY 44
 DB 41 ANSFLEELKKGNLBERCWMENCSYBAALEVFEDREKTEFMNKY 84
 RESULT 6
 FA10_BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE OF 1-487 FROM N.A.
 RP MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence".
 RT Nucleic Acids Res. 12:4481-4492(1984).
 RN (2)
 RP SEQUENCE OF 41-180.
 RP MEDLINE=80130563; PubMed=6766735;
 RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor)".
 RT Biochemistry 19:659-667(1980).
 RN (3)
 RP REVISION TO 103.
 RP MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens".

RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RX SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RX SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).

RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Glu and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 RN [14]
 RP FUNCTION. Factor Xa is a vitamin K-dependent glycoprotein that
 RP converts prothrombin to thrombin in the presence of factor Va,
 RP calcium and phospholipid during blood clotting.
 RP -1- CATALYTIC ACTIVITY. Preferential cleavage: Arg-|-Thr and then
 RP Arg-|-Ile bonds in prothrombin to form thrombin.
 RP -1- SUBUNIT. THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 RP BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 RP MORE DISULFIDE BONDS.
 RP -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 RP GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 RP CALCIUM.
 RP -1- PTM: N- AND O-GLYCOSYLATED.
 RP -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 RP INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 RP -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 RP ANOTHER SITE, BEYOND THE GLA DOMAIN.
 RP -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 RP -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A00925; EXBO.
 DR PDB; 1APO; 31-JAN-94.
 DR PDB; 1CCF; 31-MAY-94.
 DR PDB; 1WHE; 15-MAY-97.
 DR PDB; 1WHE; 15-MAY-97.
 DR MEROPS; S01.216; -.
 DR GLYCOSULEDB; P00743; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; Glu; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00659; GLA; 1.
 DR SMART; SM00020; Tryp_spec; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS02400; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_SER; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KW Glycine-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23 POTENTIAL.

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FT PROBE 24 40 FACTOR X LIGHT CHAIN.
FT CHAIN 41 180 FACTOR X HEAVY CHAIN.
FT CHAIN 183 492 ACTIVATION PEPTIDE.
FT PROBE 183 233 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN 234 492 MAY BE REMOVED BUT IS NOT NECESSARY FOR
FT PROBE 476 492 ACTIVATION.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT_SITE 275 492 CHARGE RELAY SYSTEM.
FT ACT_SITE 321 492 CHARGE RELAY SYSTEM.
FT ACT_SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 51.8%; Score 99; DB 1; Length 492;
Best Local Similarity 43.2%; Pred. No. 1.2e-09;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFKXLRGSLKXKXKXQCFXKAFKFKAXKTKLFWIXY 44
Db 41 ANSFLFVKGNGNLERECLEBACSLBAREVFEDEQTDERWSKY 84

RESULT 7
PRTC_PTC STANDARD; PRT; 459 AA.
AC Q9GHP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoprotechomoin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
DE PROC.
OS Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domain."
RU Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma: synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the Glu domain. This Glu-independent binding
CC site is necessary for the recognition of the

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CC thrombin-thrombomodulin complex.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF191307; AAC28380.1; -.
CC HSP; P04070; IPCU.
CC MEROPS; S01.218; -.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR002383; Glu_blood.
CC InterPro; IPR001254; Ser_protease_Try.
CC InterPro; IPR002294; VitK_dep_Glu.
CC Pfam; PF00008; EGF_2.
CC Pfam; PF00089; trypsin_1.
CC Pfam; PF00594; Gla; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00181; EGF_2.
CC SMART; SM00001; EGF_like; 2.
CC SMART; SM00069; Gla; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01187; EGF_Ca; 1.
CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC SIGNAL. 1 18
CC PROBE 19 41 BY SIMILARITY.
CC CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
CC CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
CC SIMILARITY).
CC CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
CC SIMILARITY).
CC PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
CC SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
CC SIMILARITY).
CC DOMAIN 96 131 EGF-LIKE 1.
CC DOMAIN 135 175 EGF-LIKE 2.
CC DOMAIN 214 459 SERINE PROTEASE.
CC MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).

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FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

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Query Match 51.3%; Score 98; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 1.6e-09;
Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRQSLKRCXKXQCSFXAFAFKDAXRTKLFWISY 44
Db 42 ANGLEELRPSLERCKEETCTDEBARERFQNTENTWAFMSKY 85

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RESULT 8

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TMG1_HUMAN STANDARD; PRT; 218 AA.

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AC 014668;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
rich Gla protein 1) (proline-rich gamma-carboxyglutamic acid protein
1).
GN PRG1 OR TMG1 OR PRGP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; Pubmed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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CC -----
CC EMBL; AF009242; AAB67070.1; .
CC HSSP; P00740; ICFH.
CC GENE; HGNC:9469; PRG1.
CC MIM; 604428; .
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR000294; VltK_dep_GLA.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00001; GLABLOOD.

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DR SMART; SMO0069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION, 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 21 83 PROTEIN 1.
FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 24 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

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Query Match 50.8%; Score 97; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 1.2e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRQSLKRCXKXQCSFXAFAFKDAXRTKLFWISY 44
Db 21 ANGFEEIRQGNIERCKEETCTDEBARERFQNTENTWAFMSKY 64

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RESULT 9

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PRTC_MOUSE STANDARD; PRT; 461 AA.

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AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=92316897; Pubmed=1618739;
RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA."
RL J. Biochem. 111:491-495(1992).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=98152576; Pubmed=9493582;
RA Jalbert L.R., Rosen E.D., Liesens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
anticoagulant protein C."
RL Thromb. Haemost. 79:310-316(1998).
RN 3;
RP SEQUENCE OF 274-434 FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=94318474; Pubmed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
RT "A comparative study of partial primary structures of the catalytic
region of mammalian protein C."
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIII
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and VIIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

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CC	-I-	PYW:	THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC	GUD RESIDUES	ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.	
CC	MISCELLANEOUS:	CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO	
CC	AOTHER SITE,	BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING	
CC	SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.		
CC	-I-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.	
CC	-I-	SIMILARITY: CONSTAINS 2 EGF-LIKE DOMAINS.	
CC	--		
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CC	--		
DR	EMBL;	D10445; BAAD0325.1; -.	
DR	EMBL;	AF034569; AACG3795.1; -.	
DR	EMBL;	D43755; BAA07812.1; -.	
DR	PIR;	JX0210; JX0210.	
DR	HSSP;	P04070; 1PCU.	
DR	MEDIPS;	SOL_218; -.	
DR	MCD;	MGJ:97721; Proc.	
DR	InterPro;	IIPRO00152; Asx_hydroxyl.	
DR	InterPro;	IIPRO0114; Chymotrypsin.	
DR	InterPro;	IIPRO00561; EGF-like.	
DR	InterPro;	IIPRO01881; EGF_Ca.	
DR	InterPro;	IIPRO02383; GLA_blood.	
DR	InterPro;	IIPRO01254; Ser_protease_Try.	
DR	InterPro;	IIPRO0294; Vlck_dep_GLA.	
DR	Pfam;	PF00008; EGF_2.	
DR	Pfam;	PF00089; trypsin; 1.	
DR	Pfam;	PF00594; gla; 1.	
DR	PRINTS;	PRQ0722; CHYMOTRYPSIN.	
DR	SMART;	SMO0001; GLABLOOD.	
DR	SMART;	SMO0179; EGF_CA; 1.	
DR	SMART;	SMO0001; EGF_like; 1.	
DR	SMART;	SMO0069; GLA; 1.	
DR	SMART;	SMO0020; Tryp_Spc; 1.	
DR	PROSITE;	PS00010; ASK_HYDROXYL; 1.	
DR	PROSITE;	PS00022; EGF_1; 1.	
DR	PROSITE;	PS01186; EGF_2; 2.	
DR	PROSITE;	PS01187; EGF_CA; 1.	
DR	PROSITE;	PS00014; GLUT_CARBOXYLATION; 1.	
DR	PROSITE;	PS0240; TRYPSIN_DOM; 1.	
DR	PROSITE;	PS00134; TRYP SIN HIS; 1.	
KW	Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; EGF-like domain; Repeat; Endothelial cell; Hydrilase; Signal.		
FT	SIGNAL	1 33 BY SIMILARITY.	
FT	CHAIN	34 41 PROTEIN C LIGHT CHAIN (BY SIMILARITY).	
FT	CHAIN	199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).	
FT	PEPTIDE	199 212 ACTIVATION PEPTIDE (BY SIMILARITY).	
FT	SITE	212 213 CLEAVEAGE (BY THROMBIN) (BY SIMILARITY).	
FT	DOMAIN	96 131 BEF-LIKE 1.	
FT	DOMAIN	135 175 BEF-LIKE 2.	
FT	MOD_RES	213 461 SERINE PROTEASE. GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	48 48 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	55 55 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	57 57 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	60 60 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	61 61 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	66 66 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	

FT	MOD_RES	67	67	(BY SIMILARITY)
FT	MOD_RES <td>70</td> <td>70</td> <td>GAMMA-CARBOXYGLUTAMIC ACID</td>	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES <td>70</td> <td>70</td> <td>(BY SIMILARITY)</td>	70	70	(BY SIMILARITY)
FT	MOD_RES <td>112</td> <td>112</td> <td>GAMMA-CARBOXYGLUTAMIC ACID</td>	112	112	GAMMA-CARBOXYGLUTAMIC ACID
FT	ACT_SITE <td>253</td> <td>253</td> <td>(BY SIMILARITY)</td>	253	253	(BY SIMILARITY)
FT	ACT_SITE <td>299</td> <td>299</td> <td>GAMMA-CARBOXYGLUTAMIC ACID</td>	299	299	GAMMA-CARBOXYGLUTAMIC ACID
FT	ACT_SITE <td>402</td> <td>402</td> <td>(BY SIMILARITY)</td>	402	402	(BY SIMILARITY)
FT	DISULFID <td>58</td> <td>63</td> <td>HYDROXYATION (BY SIMILARITY)</td>	58	63	HYDROXYATION (BY SIMILARITY)
FT	DISULFID <td>91</td> <td>110</td> <td>CHARGE RELAY SYSTEM.</td>	91	110	CHARGE RELAY SYSTEM.
FT	DISULFID <td>100</td> <td>105</td> <td>CHARGE RELAY SYSTEM.</td>	100	105	CHARGE RELAY SYSTEM.
FT	DISULFID <td>104</td> <td>119</td> <td>CHARGE RELAY SYSTEM.</td>	104	119	CHARGE RELAY SYSTEM.
FT	DISULFID <td>121</td> <td>130</td> <td>(BY SIMILARITY)</td>	121	130	(BY SIMILARITY)
FT	DISULFID <td>139</td> <td>150</td> <td>(BY SIMILARITY)</td>	139	150	(BY SIMILARITY)
FT	DISULFID <td>146</td> <td>159</td> <td>(BY SIMILARITY)</td>	146	159	(BY SIMILARITY)
FT	DISULFID <td>161</td> <td>174</td> <td>(BY SIMILARITY)</td>	161	174	(BY SIMILARITY)
FT	DISULFID <td>182</td> <td>319</td> <td>INTERCHAIN (BY SIMILARITY)</td>	182	319	INTERCHAIN (BY SIMILARITY)
FT	DISULFID <td>238</td> <td>254</td> <td>(BY SIMILARITY)</td>	238	254	(BY SIMILARITY)
FT	DISULFID <td>373</td> <td>387</td> <td>(BY SIMILARITY)</td>	373	387	(BY SIMILARITY)
FT	DISULFID <td>398</td> <td>426</td> <td>(BY SIMILARITY)</td>	398	426	(BY SIMILARITY)
FT	CARBOHYD <td>214</td> <td>214</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL)</td>	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD <td>290</td> <td>290</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL)</td>	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD <td>355</td> <td>355</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL)</td>	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CONFLICT <td>328</td> <td>328</td> <td>MISSING (IN REF. 2).</td>	328	328	MISSING (IN REF. 2).
FT	CONFLICT <td>393</td> <td>393</td> <td>N -> D (IN REF. 2).</td>	393	393	N -> D (IN REF. 2).
SO	SEQUENCE <td>461 AA;</td> <td>51945 MW; 53FPA0D85B194D6E CRC64;</td> <td></td>	461 AA;	51945 MW; 53FPA0D85B194D6E CRC64;	
Query Match		50.8%;	Score 97; DB 1; Length 461;	
Best Local Similarity		45.5%;	Pred. No. 2,4e-09;	
Matches	20; Conservative	4;	Mismatches 20; Indels	0; Gaps
Qy	1	ANAFXXLRQGSILRXCKXXQCSFXXAFYIFDXAKRTKLFWISY	44	
Db	42	ANSFLFEMRPESLERECMEICDFFEEAKQELFQVEDTTLAFWKY	85	
RESULT 10				
PRTC_RAT				
ID	PRTC_RAT	STANDARD;	PRT;	461 AA.
AC	P31394;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)			
DE	(Autoproteolytic cleavage)			
DE	(Anticoagulant protein C) (blood coagulation factor XIV).			
GN	PROC.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Liver;			
RX	MEDLINE=92329550; PubMed=1627650;			
RA	Okafuji T., Maekawa K., Nawa K., Marumoto Y.;			
RT	"The cDNA cloning and mRNA expression of rat protein C.";			
RU	Biochim. Biophys. Acta 1131:329-332 (1992).			
CC	- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT			
CC	REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA			
CC	IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.			
CC	- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va			
CC	and VIIa.			
CC	- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED			
CC	INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE			
CC	BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A			
CC	TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS			
CC	REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS			
CC	STRONGLY PROMOTED BY THROMBOMODULIN.			
CC	- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.			
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME			
CC	GU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.			

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 DR EMBL: X64336, CAA45617.1, -.
 DR PIR: S18994, S18994.
 DR PIR: S24312, S24312.
 DR HESP: P04070, 1PCU.
 DR MEROPS: S01.218, -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008, EGF_2.
 DR Pfam: PF00089, trypsin_1.
 DR Pfam: PF00594, gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00017; EGF_CA_1.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01166; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS_1.
 DR PROSITE: PS00135; TRYPSIN_SER_1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70

FT MOD_RES 112 112 (BY SIMILARITY).
 FT ACT_SITE 254 254 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
 FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 110 BY SIMILARITY.
 FT DISULFID 100 105 BY SIMILARITY.
 FT DISULFID 104 119 BY SIMILARITY.
 FT DISULFID 121 130 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 146 159 BY SIMILARITY.
 FT DISULFID 161 174 BY SIMILARITY.
 FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 239 255 BY SIMILARITY.
 FT DISULFID 373 387 BY SIMILARITY.
 FT DISULFID 398 426 BY SIMILARITY.
 FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364BDADC5 CRC64;
 Query Match 50.3%; Score 96; DB 1; Length 461;
 Best Local Similarity 45.3%; Pred. No. 3.7e-09;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGGSLKRXCKXXQCFXAFIPKDXARTKLPISY 44
 DB 42 ANSFLEERFAGSLERECHMEETDEEAOEIFONVEDTLAFIKY 85
 ID PA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 RL human coagulation factor X.";
 RN Gene 99:291-294(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;
 RA Leytue S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RL protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Pung M.R., Hay C.W., McGillicray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";


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FT MOD RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .)
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .)
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .)
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .)
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .)
FT ACT SITE 276 276 /FTID=CAR 000013.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 50.3%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 3.9e-09;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLXLROGSLRXCKXOCSPFXAFXPIDARTLPMYSY 44
DB 41 ANSFLEMKKHLERECMEETCSYEAREVFEEDSDKTNEFMNKY 84

RESULT 12
THRB HUMAN STANDARD; PRT; 622 AA.
AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RX MEDLINE=88077877; PubMed=2825773;
RA Degen S.J.F., Davie E.W.;
RT "Nucleotide sequence of the gene for human prothrombin."
RL Biochemistry 26:6165-6177(1987).
RN [2]
RX SEQUENCE FROM N.A., AND VARIANT MET-165.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toch E.J., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE OF 8-622 FROM N.A.
RX MEDLINE=83231469; PubMed=6305407;
RA Degen S.J.F., McIllivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene
RT coding for human prothrombin."
RL Biochemistry 22:2087-2097(1983).
RN [4]
RX SEQUENCE OF 44-314.
RX MEDLINE=77193964; PubMed=266717;
RA Walz D.A., Hewett-Evmett D., Seegers W.H.;
RT "Anticoagulant sequence of human prothrombin fragments 1 and 2."
RL Proc. Natl. Acad. Sci. U.S.A. 74:1965-1972(1977).
RN [5]
RX SEQUENCE OF 315-622.
RX MEDLINE=77207112; PubMed=873923;
RA Bukowski R.J., Elion J., Downing M.R., Mann K.G.;
RT "Primary structure of human prothrombin 2 and alpha-thrombin."
RL J. Biol. Chem. 252:4942-4957(1977).
RN [6]
RX PROCESSING.
RX MEDLINE=87008532; PubMed=3759958;
RA Rabiet M.J., Blachill A., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
RT activation in human plasma."
RL J. Biol. Chem. 261:13210-13215(1986).
RN [7]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=90059942; PubMed=2583108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin:
RT interaction with D-Phe-Pro-Arg chloromethylketone and significance of
RT the Tyr-Pro-Tip insertion segment."
RL EMBO J. 8:3467-3475(1989).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=90327074; PubMed=2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RA Rottsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-
RT thrombin."
RL Science 249:277-280(1990).
RN [9]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94350942; PubMed=8071320;
RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
RA Correa P.E., Fenton J.W. II, Tulinsky A.;
RT "Crystallographic structure of human gamma-thrombin."
RL J. Biol. Chem. 269:22000-22006(1994).
RN [10]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97357286; PubMed=9214615;
RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
RA Esmen C.T., Stubbs M.T.;
RT "The thrombin E192Q-BPI complex reveals gross structural
RT rearrangements: implications for the interaction with antithrombin
RT and thrombomodulin."
RL EMBO J. 16:2977-2984(1997).
RN [11]
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
RX MEDLINE=99162521; PubMed=10051558;
RA Guinto E.R., Gaccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases."
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
RN [12]
RX VARIANT BARCELONA.
RX MEDLINE=87037379; PubMed=3771562;
RA Rabiet M.-J., Furie B.C., Furie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
RT for arginine at residue 273."
RL J. Biol. Chem. 261:15045-15048(1986).
RN [13]
RX VARIANT FRANKFURT.
RX MEDLINE=95313001; PubMed=7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.W., Scharer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
RT substitution of Glu-466 by Ala."
RL Thromb. Haemost. 73:203-209(1995).
RN [14]
RX VARIANTS HIMI-1 AND HIMI-2.
RX MEDLINE=93043342; PubMed=1421398;
RA Morishita E., Saito W., Kumabeshiri I., Asakura H., Matsuoka T.,
RA Yamaguchi K.;
RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
RT prothrombin molecules (Met-337-->Thr and Arg-388-->His)."
RL Blood 80:2275-2280(1992).
RN [15]
RX VARIANT PADUA-1.
RX MEDLINE=95169898; PubMed=7865694;
RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
RT "Prothrombin Padua I: incomplete activation due to an amino acid
RT substitution at a factor Xa cleavage site."
RL Blood Coagul. Fibrinolysis 5:841-844(1994).
RN [16]
RX VARIANT QUICK-1.
RX MEDLINE=89207504; PubMed=3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysprothrombin

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RT thrombin Quick I: substitution of cysteine for arginine-382."
 RL Biochemistry 27:9160-9165(1988).
 RN [17]
 RP VARIANT QUICK-2.
 RX MEDLINE=89247398; PubMed=2719946;
 RA Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 RT thrombin Quick II alters primary substrate specificity."
 RL Biochemistry 28:2078-2082(1989).
 RN [18]
 RP VARIANT SALAKTA.
 RX MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 RT reduces the fibrinogen clotting activity and the esterase activity."
 RL Biochemistry 31:7457-7462(1992).
 RN [19]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 RT that impairs the fibrinogen clotting activity of derived thrombin
 RT Tokushima."
 RL Biochemistry 26:1117-1122(1987).
 RN [20]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87101511; PubMed=3801671;
 RA Inomoto T., Shirakami A., Kawauchi S., Shigeakiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 RT derived from a variant of human prothrombin."
 RL Blood 69:565-569(1987).
 RN [21]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=92256895; PubMed=1349838;
 RA Iwahana H., Yoshimoto K., Shigeakiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 RT Tokushima. The application of PCR-SSCP for the genetic and molecular
 RT analysis of dysprothrombinemia."
 RL Int. J. Hematol. 55:93-100(1992).
 RN [22]
 RP VARIANT TYPE-3.
 RX MEDLINE=83204687; PubMed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 RT type 3 (157 glu leads to lys) and the localization of a third
 RT thrombin cleavage site."
 RL Br. J. Haematol. 54:245-254(1983).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Gly: activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER, FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 CC DYSPROTHROMBINEMIA.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.

CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
 CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 CC NOT
 Query Match 49.2%; Score 94; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred. No. 1,1e-08;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ANAPFLXLRQSLGRXCKXQCSFXXAFIFPDARTKLFMTSY 44
 DB 44 ANTFLEVRKGLNRECEVETCSYEAFEALESSTATDVFAKY 87
 RESULT 13
 THRB_RAT
 ID THRB_RAT STANDARD; PRT; 617 AA.
 AC P18292;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN F2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=90332426; PubMed=2377469;
 RA Dihanich M., Monard D.;
 RT "cDNA sequence of rat prothrombin."
 RL Nucleic Acids Res. 18:4251-4251(1990).
 RN [2]
 RP SEQUENCE OF 383-617 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., Macgillivray R.T.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Gly: activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -

Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFIXLROGSLRXKXOCSPYXAFYIFKQAXRTKLEWISY 44
 ||| |||:| |||:| |||
 Db 20 ANEFLEELRQGTIERECMEICSYIEVKEVEFENKEKTFMFKGY 63
 ||| |||:| |||:| |||

Search completed: March 19, 2003, 14:52:49
 Job time : 6.625 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10gln28pne

Sequence: 1 ANAFIXLRGSLRXGCKX.....XXAFXIKDAXRTKLFWISY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	701	4	Q96PQ8
2	111	58.1	446	1	Q61109
3	97	50.8	460	11	Q91WN8
4	94	49.2	100	4	015253
5	91	47.6	460	11	Q99PC6
6	90	47.1	482	11	Q63207
7	88	46.1	456	6	Q9TRR0
8	88	46.1	469	6	Q9GMD9
9	88	46.1	481	11	054740
10	88	46.1	481	11	Q99L32
11	88	46.1	481	11	Q88947
12	80	41.9	456	4	Q14316
13	80	41.9	461	6	Q95ND7
14	79	41.4	461	6	Q95ND6
15	79	41.4	49	6	Q95ME8
16	73	38.2	179	4	Q87AS3

17	73	38.2	198	11	Q8R182	Q8R182 mus musculus
18	72	37.7	138	6	Q28994	Q28994 sus scrofa
19	72	37.7	608	13	Q9PTW7	Q9PTW7 struthio ca
20	69	36.1	607	13	Q91001	Q91001 gallus gall
21	67	35.1	433	13	Q90TK1	Q90TK1 brachydanio
22	67	35.1	399	11	Q9COW3	Q9COW3 mus musculus
23	64	33.5	399	13	P82807	P82807 notechis sc
24	62	32.5	98	13	Q9NSD0	Q9NSD0 homo sapien
25	62	32.5	650	4	Q16519	Q16519 homo sapien
26	62	32.5	650	4	Q16519	Q16519 homo sapien
27	57.5	30.1	542	5	Q8T613	Q8T613 halocynthia
28	55.5	29.1	431	10	Q94EY5	Q94EY5 arabidopsis
29	55.5	29.1	492	10	Q9SMJ7	Q9SMJ7 cicier ariet
30	55.5	29.1	543	10	Q9MB23	Q9MB23 arabidopsis
31	55.5	29.1	576	10	Q9C9U4	Q9C9U4 arabidopsis
32	55.5	29.1	589	10	Q9LMS2	Q9LMS2 arabidopsis
33	55	28.8	25	11	Q9QVH6	Q9QVH6 rattus sp.
34	54.5	28.5	196	10	Q04284	Q04284 selaginella
35	53.5	28.0	459	10	Q9SE22	Q9SE22 oryza sativ
36	53	27.7	673	11	Q61592	Q61592 mus musculu
37	53	27.7	674	11	Q99K57	Q99K57 mus musculu
38	52.5	27.5	506	10	Q9SEF0	Q9SEF0 oryza sativ
39	52.5	27.5	506	10	Q9SE23	Q9SE23 oryza sativ
40	52.5	27.5	567	10	Q8W4J2	Q8W4J2 arabidopsis
41	51.5	27.0	510	10	Q9MB22	Q9MB22 arabidopsis
42	51.5	27.0	619	10	Q9LV37	Q9LV37 arabidopsis
43	51	26.7	674	11	Q63772	Q63772 rattus sp.
44	51	26.7	678	4	Q14393	Q14393 homo sapien
45	49.5	25.9	588	10	Q9LW33	Q9LW33 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q96PQ8	PRELIMINARY;	PRT;	701 AA.
AC	Q96PQ8;			
DT	01-DEC-2001 (TREMURel. 19, Created)			
DT	01-DEC-2001 (TREMURel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMURel. 20, Last annotation update)			
DE	Factor VII active site mutant immunocoujugate.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_taxonomy:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21477448; PubMed=11593034;			
RA	Hu Z., Garen A.;			
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR	EMBL; AF272774; AKS58686.1; -			
DR	InterPro; IPR000152; Aex_hydroxyl.			
DR	InterPro; IPR000561; BGF-like.			
DR	InterPro; IPR00742; BGF_2.			
DR	InterPro; IPR01881; EGF_Ca.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR001254; Ser_protease_Try.			
DR	InterPro; IPR000294; VltK_dep_GLA.			
DR	Pfam; PF00008; EGF_2.			
DR	Pfam; PF00594; Gla_1.			
DR	Pfam; PF00047; Ig_2.			
DR	Pfam; PF00089; trypsin_1.			
DR	SMART; SM00181; EGF_2.			
DR	PROSITE; PS00012; ASX_HYDROXYL; UNKNOWN_1.			
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.			
DR	PROSITE; PS01187; EGF_CA; UNKNOWN_1.			
DR	PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.			
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.			
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
Query Match 81.7%; Score 156; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 1.9e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ANAFLLXLRQGSLLRXCKXKCCSFXKAFIFPDARTKLFWISY 44
DB 61 ANAFLEELRPGSLERCKECCSFEEAREIFPDARTKLFWISY 104
RESULT 2
ID Q61109 PRELIMINARY; PRT; 446 AA.
AC Q61109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idsogte E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.,
RT "Characterization of a cDNA encoding murine coagulation factor VII.",
RL Thromb. Haemost. 75:481-487 (1996).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U4795; AAC52570.1; -.
DR HESP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser. protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00025; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FDD09BEFDA6870 CRC64;
Query Match 58.1%; Score 111; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 3.2e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
QY 1 ANAFLLXLRQGSLLRXCKXKCCSFXKAFIFPDARTKLFWISY 44
DB 42 ANSLLEELMPGSLERCKNECCSFEEAREIFKSPERTQFWIV 85
RESULT 3
ID Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX Strausberg R.,
RA Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser. protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLUT CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F265B8FCC274 CRC64;
Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.4e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
QY 1 ANAFLLXLRQGSLLRXCKXKCCSFXKAFIFPDARTKLFWISY 44
DB 42 ANSFLLEMRPGSLERCKMEICDFEEAOEIFQNVDTLAFWIKY 85
RESULT 4
ID Q15253 PRELIMINARY; PRT; 100 AA.
AC Q15253;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;

RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PRL.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; Gla; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Signal.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; PDESD0174E1P6FE CRC64;
Query Match 49.2%; Score 94; DB 4; Length 100;
Best Local Similarity 38.6%; Pred. No. 1.1e-09;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
OY 1 ANAPLXLROGSLRXCKXKOCSEFXAXFIFKDXARTLFWISY 44
DB 44 ANFLAEVRKGNLERECVEETCSYEAEFALSSSTATDVFWAKY 87
RESULT 5
O99PC6 PRELIMINARY; PRT; 460 AA.
AC O99PC6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC -1- TRYPsin FAMILY.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR SMART; SM00069; Gla; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC259D3ED16 CRC64;
Query Match 47.6%; Score 91; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.9e-08;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
OY 1 ANAPLXLROGSLRXCKXKOCSEFXAXFIFKDXARTLFWISY 44
DB 42 ANFLAEVRKGNLERECVEETCSYEAEFALSSSTATDVFWAKY 85
RESULT 6
O63207 PRELIMINARY; PRT; 482 AA.
ID O63207;
AC O63207;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC -1- TRYPsin FAMILY.
DR EMBL; X79807; CAAS6202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; Gla; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678B3954A638 CRC64;
Query Match 47.1%; Score 90; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 3e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;


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GN F10 OR FA10.
OS Mus musculus (Mouse).
OG Plasmid pluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00017; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00020; TRY_SPC; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRGSLRXKCKXKXCSFXKAFIFKDAKRTKLFWTSY 44
Db 41 ANSFEEFKGNLREKCMELCSYEVRREIFEDDEKTKYWTXY 84

RESULT 10
O99L32 PRELIMINARY; PRT; 481 AA.
AC O99L32.
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88B96CA0B7E7F CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRGSLRXKCKXKXCSFXKAFIFKDAKRTKLFWTSY 44
Db 41 ANSFEEFKGNLREKCMELCSYEVRREIFEDDEKTKYWTXY 84

RESULT 11
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947.
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen B.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=129SJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSB; P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; P10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 1 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EF9D271E CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAFKDXRTKLFWISY 44
DB 41 ANSFPEFPKKNLNERCEMEICSYEEVREIFEDDEKTKWTKY 84

RESULT 12
Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX [Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B]) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RE Retema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

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RA Briel E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSB; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 41.9%; Score 80; DB 4; Length 456;
Best Local Similarity 42.9%; Pred. No. 2.2e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLRXCKXXQCSFXXAFKDXRTKLFWISY 44
DB 52 QGNLERCEMEKCSFEAREVFENTERITFEWKQY 86

RESULT 13
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.

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DR EMBL; AB062466; BAB58885.1; JOINED.
 DR EMBL; AB062468; BAB58885.1; JOINED.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GlA; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 KM SEQUENCE 461 AA; 5164 MW; 30C2F857C0F7F45 CRC64;

Query Match 41.9%; Score 80; DB 6; Length 461;
 Best Local Similarity 42.9%; Pred. No. 2.2e-06;
 Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 OGSIXRXXKXXQCSFXXAFKFXDAXRTKLFWISY 44
 Db 57 QGNLERCEMEKCSFEAREVVENTERTTEFWKQY 91

RESULT 14

ID Q95ND6 PRELIMINARY; PRT; 461 AA.
 AC Q95ND6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Coagulation factor XI.
 GN F9.
 OS Pan troglodytes (Hominidae).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=505;
 RA Saita Y.;
 RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees";
 RL Genes Genet. Syst. 0:0-0(2001).
 DR EMBL; AB062471; BAB58886.1; -.
 DR EMBL; AB062459; BAB58886.1; JOINED.
 DR EMBL; AB062461; BAB58886.1; JOINED.
 DR EMBL; AB062463; BAB58886.1; JOINED.
 DR EMBL; AB062465; BAB58886.1; JOINED.
 DR EMBL; AB062467; BAB58886.1; JOINED.
 DR EMBL; AB062469; BAB58886.1; JOINED.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GlA; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 KM SEQUENCE 461 AA; 51695 MW; 8F5A69A5250F65B5 CRC64;

Query Match 41.9%; Score 80; DB 6; Length 461;
 Best Local Similarity 42.9%; Pred. No. 2.2e-06;
 Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 OGSIXRXXKXXQCSFXXAFKFXDAXRTKLFWISY 44
 Db 57 QGNLERCEMEKCSFEAREVVENTERTTEFWKQY 91

RESULT 15

ID Q95ME8 PRELIMINARY; PRT; 49 AA.
 AC Q95ME8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Coagulation factor IX (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizlaria M.N., Amara E.J.;
 RT "Partial sequence of bovine F9 coding gene."
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF394598; AAK77556.1; -.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00594; GlA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 49 AA; 6023 MW; DISC6DE9CCBA4A14 CRC64;

Query Match 41.4%; Score 79; DB 6; Length 49;
 Best Local Similarity 40.0%; Pred. No. 3.4e-07;
 Matches 14; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 10 OGSIXRXXKXXQCSFXXAFKFXDAXRTKLFWISY 44
 Db 14 QGNLERCEMEKCSFEAREVVENTERTTEFWKQY 48

Search completed: March 19, 2003, 15:13:31
 Job time : 47.3125 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLN28PHE
Perfect score: 191
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165	86.4	44	3	US-08-955-636-28
2	159	83.2	44	3	US-08-955-636-26
3	158	82.7	44	3	US-08-955-636-30
4	157	82.2	44	3	US-08-955-636-27
5	156	81.7	44	3	US-08-955-636-3
6	156	81.7	406	1	US-08-293-778-24
7	156	81.7	406	1	US-08-295-411-5
8	156	81.7	406	1	US-08-955-471-5
9	156	81.7	406	5	PCT-US92-10242-5
10	156	81.7	444	1	US-08-475-845-2
11	156	81.7	444	2	US-08-327-690-2
12	156	81.7	444	2	US-08-660-289-2
13	156	81.7	444	2	US-08-537-807-2
14	156	81.7	444	2	US-08-871-003-2
15	156	81.7	444	3	US-08-464-233-2
16	156	81.7	444	4	US-09-189-607-2
17	156	81.7	444	4	US-09-378-907-2
18	156	81.7	444	5	PCT-US94-05779-2
19	156	81.7	466	1	US-07-882-202A-4
20	156	81.7	466	1	US-08-021-615A-4
21	156	81.7	466	1	US-08-321-777-4
22	156	81.7	466	4	US-09-009-217-14
23	156	81.7	466	4	US-09-009-656-14
24	156	81.7	466	3	PCT-US93-04493-4
25	150	78.5	44	3	US-08-955-636-29
26	141	73.8	41	1	US-08-229-280-4
27	122	63.9	44	3	US-08-955-636-4

28	105	55.0	139	1	US-08-330-978-2	Sequence 2, Appli
29	105	55.0	139	1	US-08-474-042-2	Sequence 2, Appli
30	105	55.0	139	1	US-08-484-558-2	Sequence 2, Appli
31	105	55.0	139	1	US-08-774-592-2	Sequence 2, Appli
32	105	55.0	437	1	US-08-487-037-2	Sequence 2, Appli
33	105	55.0	437	1	US-08-487-037-3	Sequence 3, Appli
34	105	55.0	488	1	US-08-487-037-1	Sequence 1, Appli
35	99	51.8	44	3	US-08-955-636-18	Sequence 18, Appli
36	99	51.8	487	1	US-08-469-486-53	Sequence 53, Appli
37	99	51.8	487	2	US-08-469-658-53	Sequence 53, Appli
38	99	51.8	492	1	US-08-469-486-2	Sequence 2, Appli
39	99	51.8	492	2	US-08-469-658-2	Sequence 2, Appli
40	97	50.8	44	3	US-08-955-636-24	Sequence 24, Appli
41	96	50.3	448	1	US-08-295-411-3	Sequence 3, Appli
42	96	50.3	448	2	US-08-955-471-3	Sequence 3, Appli
43	96	50.3	448	5	PCT-US92-10068-1	Sequence 1, Appli
44	96	50.3	448	5	PCT-US92-10242-3	Sequence 3, Appli
45	95	49.7	44	3	US-08-955-636-25	Sequence 25, Appli

ALIGNMENTS

```
RESULT 1
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      86.4%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.1e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANAFLXXLRQGSIXKXCKXCSFXAXIFPDAXRTLFWISY 44
Db      1 ANAFLXXLRQGSIXKXCKXCSFXAXIFPDAXRTLFWISY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 83.2%; Score 159; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.2e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFIIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 3
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseuten, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-30

Query Match 82.7%; Score 158; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 4.8e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFIIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 4
US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseuten, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-27

Query Match 82.2%; Score 157; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFIIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 5
US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseuten, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-3

Query Match 81.7%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFIIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 6
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560

GENERAL INFORMATION:

APPLICANT: Nicolaisen, Else M.

APPLICANT: Bjorn, Soren E.

APPLICANT: Wiberg, Finn C.

TITLE OF INVENTION: MODIFIED FACTOR VII/Viia

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,778

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509

FILING DATE:

APPLICATION NUMBER: DK 3235/87

FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/434,149

FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: PCT/DK88/00103
: FILING DATE: 24-JUN-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/898,248
: FILING DATE: 12-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Agria, Cheryl H.
: REGISTRATION NUMBER: 34,086
: REFERENCE/DOCKET NUMBER: 3129,224-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-867-0298
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-293-778-24

```

```

Query Match      81.7%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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```

Qy 1 ANAFLLXLRGSLXRXCKXQCSFXXAFIFPDAXRTKLFWISY 44
Db 1 ANAFLLYLRPGSLRYCKRYQCSFYARYFRDAVRTKLFWISY 44

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```

RESULT 7
: Sequence 5, Application US/08295411
: Patent No. 5679639
: GENERAL INFORMATION:
: APPLICANT: Griffin, John H.
: APPLICANT: Mesters, Rolf M.
: TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
: TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
: TITLE OF INVENTION: for Inhibiting Coagulation
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Office of Patent Counsel, The Scripps
: ADDRESSEE: Research Institute
: STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/295,411
: FILING DATE: 22-AUG-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: TSRI263,0C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid

```

```

: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note= "Factor VII light chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note= "Factor VII Heavy Chain"
: US-08-295-411-5

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```

Query Match      81.7%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRGSLXRXCKXQCSFXXAFIFPDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLRECKEBCQSFPEARIFPDAXRTKLFWISY 44

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RESULT 8
: Sequence 5, Application US/08955471
: Patent No. 5968751
: GENERAL INFORMATION:
: APPLICANT: Griffin, John H.
: APPLICANT: Mesters, Rolf M.
: TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
: TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
: TITLE OF INVENTION: for Inhibiting Coagulation
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Office of Patent Counsel, The Scripps
: ADDRESSEE: Research Institute
: STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/955,471
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/295,411
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: TSRI263,0C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152

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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153...406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 81.7%; Score 156; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 1 ANAFLEELRPGSLERCKEKCQCSFEAREIFDAXRTKLFWISY 44

RESULT 9
PCT-US92-10242-5

Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153...406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5
Query Match 81.7%; Score 156; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ANAFXXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 1 ANAFLEELRPGSLERCKEKCQCSFEAREIFDAXRTKLFWISY 44

RESULT 10
US-08-475-845-2

Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 19952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2
Query Match 81.7%; Score 156; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ANAFXXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEKCQCSFEAREIFDAXRTKLFWISY 82
RESULT 11
US-08-327-690-2

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; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match      81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY      1 ANAFLLXLRGSLKRXCKXQCSFXAIFKDXARTLFWISY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      39 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTLFWISY 82

RESULT 13
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEEOCSFEAREIFPDARTKLFWISY 82

RESULT 14
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEEOCSFEAREIFPDARTKLFWISY 82

RESULT 15
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 81.7%; Score 156; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEEOCSFEAREIFPDARTKLFWISY 82

Search completed: March 19, 2003, 15:16:14
Job time : 9.75 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10Gln28PHE
Perfect score: 191
Sequence: 1 ANAFLLXLRQGSILRXCKXX.....XAXAFIFKDXRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60 PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	406	9 US-10-109-498-1	Sequence 1, Appli
2	97	50.8	419	9 US-10-182-263-6	Sequence 6, Appli
3	92	48.2	419	9 US-10-182-263-3	Sequence 3, Appli
4	92	48.2	419	9 US-10-182-263-4	Sequence 4, Appli
5	92	48.2	419	9 US-10-182-263-5	Sequence 5, Appli
6	81	42.4	419	9 US-10-182-263-1	Sequence 1, Appli
7	81	42.4	419	9 US-09-978-917A-4	Sequence 4, Appli
8	81	42.4	461	9 US-10-182-263-2	Sequence 2, Appli
9	81	42.4	461	9 US-09-978-917A-2	Sequence 2, Appli
10	80	41.9	415	10 US-09-118-748-2	Sequence 2, Appli
11	80	41.9	461	9 US-10-132-829-5	Sequence 5, Appli
12	80	41.9	461	10 US-09-884-901-3	Sequence 3, Appli
13	66.5	34.8	96	9 US-09-759-130B-313	Sequence 313, App
14	66.5	34.8	209	9 US-09-759-130B-312	Sequence 312, App
15	66.5	34.8	226	9 US-09-759-130B-310	Sequence 310, App
16	51.5	27.0	95	9 US-09-759-130B-356	Sequence 356, App
17	51.5	27.0	208	9 US-09-759-130B-355	Sequence 355, App
18	51.5	27.0	225	9 US-09-759-130B-353	Sequence 353, App
19	45.5	23.8	729	9 US-10-145-396-11	Sequence 11, Appli

20	44.5	23.3	347	10 US-09-780-053-4	Sequence 4, Appli
21	44.5	23.3	730	9 US-10-145-396-12	Sequence 12, Appli
22	44.5	23.3	730	10 US-09-780-053-2	Sequence 2, Appli
23	41	21.5	88	10 US-09-811-284-194	Sequence 194, App
24	40	20.9	240	9 US-09-782-504-4	Sequence 4, Appli
25	40	20.9	447	10 US-09-815-242-13490	Sequence 13490, A
26	40	20.9	447	10 US-09-815-242-13612	Sequence 13612, A
27	40	20.9	447	10 US-09-735-564-2	Sequence 2, Appli
28	39	20.4	115	9 US-09-883-152-21	Sequence 21, Appli
29	39	20.4	115	9 US-09-986-480-192	Sequence 192, App
30	39	20.4	130	9 US-09-986-480-345	Sequence 345, App
31	39	20.4	254	9 US-10-104-019-21	Sequence 21, Appli
32	39	20.4	873	9 US-10-200-154-2	Sequence 2, Appli
33	39	20.4	873	10 US-09-954-043-2	Sequence 2, Appli
34	38.5	20.2	111	10 US-09-899-896-7	Sequence 7, Appli
35	38.5	20.2	206	10 US-09-970-711-13	Sequence 13, Appli
36	38	19.9	47	10 US-09-739-254-109	Sequence 109, App
37	38	19.9	47	10 US-09-904-615-109	Sequence 109, App
38	38	19.9	176	9 US-10-078-770-106	Sequence 106, App
39	38	19.9	273	9 US-09-764-868-968	Sequence 968, App
40	38	19.9	333	9 US-09-738-626-5683	Sequence 5683, App
41	38	19.9	400	9 US-10-078-770-114	Sequence 114, App
42	38	19.9	608	10 US-09-908-664-5	Sequence 5, Appli
43	38	19.9	1266	9 US-09-931-969A-2	Sequence 2, Appli
44	38	19.9	1266	9 US-10-079-699-2	Sequence 2, Appli
45	38	19.9	1266	10 US-09-757-781-63	Sequence 63, Appli

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/261,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      81.7%; Score 156, DB 9, Length 406;
Best local Similarity 95.5%; Pred. No. 5.3e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRQGSILRXCKXXCSPXAXAFIFKDXRTLFWISY 44
Db 1 ANAFLLXLRQGSILRXCKXXCSPXAXAFIFKDXRTLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
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Oy      1 ANAFXXLRGSLKRXCKXOCSFFXXAFXIFDXDARTKLFW 41
        1 ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 ANSPLEELRHGSLERECIEICDFEEALAEIFEDVDOTLAFW 41

RESULT 6
US-10-182-263-1
Sequence 1, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 419
TYPE: PRT

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ORGANISM: Homo sapiens
US-10-182-263-1

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKXAFIFKDXARTKLFW 41
DB 1 ANSFLELRHSSLERECIEBICDFEAKEIFQNVDDTLAFW 41

RESULT 7

US-09-978-917A-4
Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKXAFIFKDXARTKLFW 41
DB 1 ANSFLELRHSSLERECIEBICDFEAKEIFQNVDDTLAFW 41

RESULT 8

US-10-182-263-2
Sequence 2, Application US/10182263
Publication No. US2003002354A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan B
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens
US-10-182-263-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKXAFIFKDXARTKLFW 41
DB 43 ANSFLELRHSSLERECIEBICDFEAKEIFQNVDDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens

NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKXAFIFKDXARTKLFW 41
DB 43 ANSFLELRHSSLERECIEBICDFEAKEIFQNVDDTLAFW 83

RESULT 10

US-09-118-748-2
Sequence 2, Application US/09118748A
Patent No. US20020031799A1

GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118,748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT

ORGANISM: Homo sapiens
US-09-118-748-2

Query Match
Best Local Similarity 41.9%; Score 80; DB 10; Length 415;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 10 QGSLRXCKXKXQCSFXKXAFIFKDXARTKLFWISY 44
DB 11 QGNLERECMEBKCSFEAREVFEVNTERTTFWKQY 45

RESULT 11

US-10-132-829-5
Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
FILE REFERENCE: 6627-Pa1170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          41.9% Score 80; DB 9; Length 461;
Best Local Similarity 42.9%; Pred. NO. 2.5e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 57 QGNLRECEMEKCSFEAREVFENTERTEFTWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: USFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-901-3

Query Match          41.9% Score 80; DB 10; Length 461;
Best Local Similarity 42.9%; Pred. NO. 2.5e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 57 QGNLRECEMEKCSFEAREVFENTERTEFTWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          34.8% Score 66.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. NO. 0.00013;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

Qy 2 NAF-LXXLRGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 36 NRPDLELFTPTGNLRECEMEKELCNVEAREEIFVDEBDKTIKFAWQCY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

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Query Match      34.8%; Score 66.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

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QY      2 NAF-LXXLRGSLXRCXXCSPFXAIFKDXARTKLFWISY 44
DB      36 NRPDLLEFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 79

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RESULT 15

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US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OR INVENTION: USES.
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-09-759-130B-310

```

```

Query Match      34.8%; Score 66.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 0.00031;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

```

```

QY      2 NAF-LXXLRGSLXRCXXCSPFXAIFKDXARTKLFWISY 44
DB      53 NRPDLLEFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 96

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Search completed: March 20, 2003, 13:30:11
Job time : 9.375 secs

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DR		WP1; 1999-288309/24.
XX		Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
Pt		
XX		
PS		Disclosure; Page 80; 86pp; English.
XX		
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.	
CC		
CC		
CC		
SQ	Sequence	44 AA;
Dc	Query Match	86.8%; Score 165; DB 20; Length 44; Best Local Similarity 97.7%; Pred. NO. 2e-20; Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps
Ov	1 ANAFLLXLRGSLRXCKXCOCSPFXAXEIPKDXRTKLFWISY 44 1 ANAFLLXLRGSLRXCKXCOCSPFXAXIIFKDAXRKLFWISY 44	
ID	AAY18311 standard; peptide; 44 AA. AAV18311; AAY18311; AAY18311; (first entry)	
DT	Modified GLA domain of vitamin K-dependent protein.	
DE	GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.	
KW	Homo sapiens.	
XO	Synthetic.	
OS		
FH	Key Location/Qualifiers	
FT	Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"	
FT		
FN	WO9920767-A1.	
PD	29-APR-1999.	
PF	20-OCT-1998; 98WO-US22152.	
PR	23-OCT-1997; 97US-0955636.	
PA	(MINU) UNIV MINNESOTA.	
PI	Nelbeetuen GI;	
DP	WP1; 1999-288309/24.	
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders	
PS	Disclosure; Page 80; 86pp; English.	
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the	

[illegible]

RESULT 4
 AAB36395
 ID AAB36395 standard; peptide; 44 AA.
 XX
 AC AAB36395;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GIIA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Homo sapiens.
 XX
 PN MO20006753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 P1 Neiseetuen GL;
 P1
 XX WPI; 2001-007226/01.
 XX
 DR
 XX
 PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprising modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 PS
 XX Disclosure; Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GIIA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GIIA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GIIA domain sequence, given in
 CC the exemplification of the present invention.
 CC
 SQ Sequence 44 AA;
 XX
 XX
 Query Match 83.7%; Score 159; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2e-19; Indels 0; Gaps 0;
 Matches 42; Conservative 0; Mismatches 2;
 Oy 1 ANAFLXILREGSLXRXCKXQCSFYXAXEIPFDAXRTKLFMISY 44
 |||||
 Db 1 ANAFLXILRPSGLRXCKXQCSFYXAXEIPFDAXRTKLFMISY 44
 |||||
 RESULT 5
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.
 XX
 AC AAB84870;
 XX
 DT 31-JUL-2001 (first entry)
 XX

DE Mutant blood coagulant factor VII (FVII-31).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 DT Synthetic.
 XX
 DE Key location/Qualifiers
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 PD JP2001061479-A.
 XX
 PF 13-MAR-2001.
 XX
 PR 24-AUG-1999; 99JP-0237610.
 XX
 PR 24-AUG-1999; 99JP-0237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX
 PS Claim 14; Page 20-21; 29pp; Japanese.
 XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 CC
 SQ Sequence 401 AA;
 XX
 XX
 Query Match 83.7%; Score 159; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 1.9e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 ANAFLXILREGSLXRXCKXQCSFYXAXEIPFDAXRTKLFMISY 44
 |||||
 Db 1 ANAFLXILRPSGLRXCKXQCSFYXAXEIPFDAXRTKLFMISY 44
 |||||
 RESULT 6
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.
 XX
 AC AAB84871;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 DT Synthetic.
 XX
 DE Key location/Qualifiers
 FT Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 FT Asp-Arg-Lys-Thr-Leu"
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 PN JP2001061479-A.
 XX

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PD 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
PA (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
SQ Sequence 401 AA;

Query Match 83.7%; Score 159; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXKQCSFXXAEXIFKDAKRTKLFWISY 44
Db 1 ANAFLELRGSLRCKEKCQSFEEAREIFKDAERTKLFWISY 44

RESULT 7
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX
XX AAR35764;
XX
XX 24-SEP-1993 (first entry)
XX
XX Factor VII (VII).
XX
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX exosite; catalytic activity.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..152
XX Region /note= "Factor VII light chain"
XX FT 153..406
XX Region /note= "Factor VII heavy chain"
XX FT 374..388
XX Peptide /note= "exosite 1"
XX FT 290..310
XX Peptide /note= "exosite 2"
XX FT 290..310
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 374..388
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 289..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 290..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 245..266
XX Peptide /note= "claim 9, page 138-139 describes an antibody
XX that reacts with Factor VII; fragments
XX 289-304, 290-304, 290-310, 374-388 and
XX 400-414 but not with fragment 245-266"
XX
XX WO9309804-A.

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PD 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPS RES INST.
XX
XX Griffin JH, Meesters RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide
XX antibodies - for inhibiting coagulation and assaying for the
XX presence of serine protease in fluid samples
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
XX coagulation (they prevent binding of serine protease to natural
XX substrates), esp. when admin. to give an intravascular blood
XX concn. of 0.1-100 (pref. 0.5-10) microm.
XX CB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
XX in the specification but have not yet been added to the SEQUENCE
XX LISTING.
XX
SQ Sequence 406 AA;

Query Match 83.7%; Score 159; DB 14; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXKQCSFXXAEXIFKDAKRTKLFWISY 44
Db 1 ANAFLELRGSLRCKEKCQSFEEAREIFKDAERTKLFWISY 44

RESULT 8
AAW14509
ID AAW14509 standard; protein; 406 AA.
XX
XX AAW14509;
XX
XX 14-MAY-1997 (first entry)
XX
XX Modified blood coagulation Factor VII (R290S).
XX
XX Blood coagulation; factor 7; mutation; modification;
XX thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 6
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 7
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 14
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 16
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 19
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 20
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 17..22
XX Disulfide-bond

```


FT	Modified-site	25	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	26	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	29	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	32..33	/note= "proteolytic site"
FT		35	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Cleavage-site	38..39	/note= "proteolytic site"
FT		42..43	/note= "proteolytic site"
FT	Cleavage-site	44..45	/note= "proteolytic site"
FT		50..61	/note= "proteolytic site"
FT	Modified-site	55..70	
FT		63	//label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Disulfide-bond	72..81	
FT		91..102	
FT	Disulfide-bond	98..112	
FT		114..127	
FT	Disulfide-bond	135..162	
FT		143..144	
FT	Cleavage-site	/note= "proteolytic site"	
FT		145	
FT	Modified-site	/note= "glycosylation site"	
FT		159..164	
FT	Disulfide-bond	178..194	
FT		193	
FT	Active-site	242	
FT		344	
FT	Active-site	290..291	
FT	Cleavage-site	/note= "proteolytic site in unmodified factor VII"	
FT		290	
FT	Misc-difference	/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT		310..329	
FT	Disulfide-bond	315..316	
FT	Cleavage-site	/note= "proteolytic site"	
FT		322	
FT	Modified-site	/note= "glycosylation site"	
FT		340..368	
FT	Disulfide-bond	341..342	
FT	Cleavage-site	/note= "proteolytic site"	
FT		392..393	
FT	Cleavage-site	/note= "proteolytic site"	
FT		396..397	
FT	Cleavage-site	/note= "proteolytic site"	
FT		402..403	
FT	Cleavage-site	/note= "proteolytic site"	
XX		US5580560-A.	
XX		03-DEC-1996.	
XX		13-NOV-1989;	89US-0434149.
XX		09-AUG-1993;	93US-0104509.
XX		13-NOV-1989;	89US-0434149.
XX		12-JUN-1992;	92US-0889248.
XX		22-AUG-1994;	94US-0293778.
XX		(NOVO) NOVO-NORDISK AS.	

PI	Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;
XX	
DR	WPI, 1997-033523/03.
PT	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability
PT	
PS	Example 3; Page -: 28pp; English.
XX	
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, CC
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and CC
CC	Lys441 by an amino acid that provides a proteolytically more stable CC
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His, CC
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating CC
CC	bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. CC
CC	The present sequence is a specific example of a modified factor VII protein.
CC	
XX	
SQ	Sequence 406 AA;
Query Match	83.7%; Score 159; DB 18; Length 406;
Best Local Similarity	72.7%; Pred.No.1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0	
Oy	1 ANAFPLXLRSGSLRXKCKKXOCSFPXAEXIFPDARTKLFWSY 44 1 AHAFLFELRPGSLBRECKECCSFEARERIPDARTKLFWSY 44
Db	
RESULT 9	
AAM14510	ID AAM14510 standard; protein; 406 AA.
XX	
XX	AAW14510;
AC	14-MAY-1997 (first entry)
DR	
XX	
DE	Modified blood coagulation Factor VII (R315S).
XX	
KW	Blood coagulation; factor 7; mutein; mutation; modification; thrombocytopenia; von Willebrand's disease; plasma substitute.
KW	
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	6 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	
FT	7 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	14 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	16 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	19 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	20 /label= OTHER
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	Disulfide-bond 17..22
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	26 /label= OTHER
FT	/label= "gamma-carboxylutamic acid"

FT	Modified-site	29	/label= OTHER
FT		/note= "gamma-carboxylutamic acid"	
FT	Cleavage-site	32..33	/note= "proteolytic site"
FT	Modified-site	35	/label= OTHER
FT		/note= "gamma-carboxylutamic acid"	
FT	Cleavage-site	38..39	/note= "proteolytic site"
FT	Cleavage-site	42..43	/note= "proteolytic site"
FT	Cleavage-site	44..45	/note= "proteolytic site"
FT		/note= "proteolytic site"	
FT	Disulfide-bond	50..61	/note= "proteolytic site"
FT	Disulfide-bond	55..70	/note= "proteolytic site"
FT	Modified-site	63	/label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Disulfide-bond	72..81	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	91..102	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	98..112	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	114..127	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	135..162	/note= "beta-hydroxy-aspartic acid"
FT	Cleavage-site	143..144	/note= "proteolytic site"
FT	Modified-site	145	/note= "proteolytic site"
FT		/note= "glycosylation site"	
FT	Disulfide-bond	159..164	/note= "glycosylation site"
FT	Disulfide-bond	178..194	/note= "glycosylation site"
FT	Active-site	193	/note= "glycosylation site"
FT	Active-site	242	/note= "glycosylation site"
FT	Active-site	344	/note= "glycosylation site"
FT	Cleavage-site	290..291	/note= "proteolytic site"
FT		/note= "proteolytic site"	
FT	Disulfide-bond	310..329	/note= "proteolytic site"
FT	Cleavage-site	315..316	/note= "proteolytic site"
FT	Misc-difference	315	/note= "proteolytic site in unmodified factor VII"
FT		/note= "native Arg315 has been substituted by Ser to	
FT		provide a proteolytically more stable peptide	
FT	Modified-site	322	/note= "glycosylation site"
FT		/note= "glycosylation site"	
FT	Disulfide-bond	340..368	/note= "glycosylation site"
FT	Cleavage-site	341..342	/note= "proteolytic site"
FT	Cleavage-site	392..393	/note= "proteolytic site"
FT	Cleavage-site	396..397	/note= "proteolytic site"
FT	Cleavage-site	402..403	/note= "proteolytic site"
FT	Cleavage-site	/note= "proteolytic site"	
XX			
PM	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	13-NOV-1989;	89US-0434149.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
DR	WPI, 1997-033523/03.		
XX			
PT	Mutated human factor VII or VIIa proteins - with amino acid		
PT	substitutions to improve proteolytic stability		

```

xx Example 4; Page -; 28pp; English.
xx
xx Modified human factor VII or VIIa proteins are stabilised against
xx proteolytic cleavage by substitution of one of the residues Lys32,
xx Lys68, Ile42, Tyr44, Phe278, Arg390, Arg304, Arg315, Tyr332 and
xx Lys441 by an amino acid that provides a proteolytically more stable
xx peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
xx Gly, Thr, Ala or Ser. The modified proteins are useful for treating
xx bleeding disorders such as thrombocytopenia and von Willebrand's
xx disease. They are also suitable for addition to plasma substitutes.
xx The present sequence is a specific example of a modified factor VII
xx protein.
xx
xx Sequence 406 AA:
xx
xx Query Match 83.7%; Score 159; DB 18; Length 406;
xx Best Local Similarity 72.7%; Pred. No. 1.9e-18;
xx Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
xx
xx 1 ANAFPLXLRREGSLMRXXCKXKQCSFXXAEXIFKDAHYTLFWISY 44
xx ||||| ||||| ||||| ||||| ||||| ||||| |||||
xx 1 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTLFWISY 44
xx
xx RESULT 10
xx AAU77745
xx ID AAU77745 standard; protein; 406 AA.
xx
xx AC AAU77745;
xx
xx DT 05-JUN-2002 (first entry)
xx
xx DE Human factor VIIa active site mutant.
xx
xx KM Factor VIIa; human; shock heat treatment; protein stability;
xx protein manufacture; protein conformation; mutant; mntein.
xx
xx OS Homo sapiens.
xx
xx OS Synthetic.
xx
xx PH Key Location/Qualifiers
xx FT Active-site 193
xx FT Active-site /note= "Member of the factor VIIa catalytic triad"
xx FT Active-site 242
xx FT Active-site /note= "Member of the factor VIIa catalytic triad"
xx FT Active-site 344
xx FT Active-site /note= "Member of the factor VIIa catalytic triad"
xx FT Misc-difference 344
xx FT /label= Gly, Met, Thr
xx FT /note= "Preferably Ala. Wild type Ser"
xx
xx PN WO200177141-A1.
xx
xx PD 18-OCT-2001.
xx
xx PF 06-APR-2001; 2001WO-DK00234.
xx
xx PR 06-APR-2000; 2000DK-0000573.
xx PR 17-APR-2000; 2000US-197650P.
xx
xx (NOVO ) NOVO NORDISK AS.
xx
xx Matchiesen F;
xx
xx PI WPI, 2001-657162/75.
xx
xx DR
xx
xx PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
xx involves a shock heat treatment -
xx
xx Disclosure; Page -; 22pp; English.
xx
xx The invention describes a method of stabilising a polypeptide involving

```

CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition, in the industrial or large scale method of
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified
 CC human factor VIIa protein, mutated at the catalytic site, described
 CC in the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been obtained using information given in the invention.

CC Sequence 406 AA;

Query Match 83.7%; Score 159; DB 22; Length 406;
 Best Local Similarity 72.7%; Pred. No. 1.9e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXAEXIFPDAXRTKLFWISY 44
 |||||
 Db 1 ANAFLLELRPGSLRCKECCSFEEAREIFDAERTKLFWISY 44

RESULT 11

AAM52171
 ID AAM52171 standard; Protein; 406 AA.

XX AC AAM52171;

XX DT 07-FEB-2002 (first entry)

XX DE Human FVII SEQ ID NO 1.

XX KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatocytic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 6 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 7 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 14 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 16 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 19 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 20 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 25 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 26 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 29 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 35 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"

FT Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"

FT

FT /note= "O-glycosylated"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Modified-site 145 /note= "N-glycosylated"
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains
 FT linked by a single disulphide bridge"

FT Modified-site 322 /note= "N-glycosylated"

FT WO200158935-A2.

FT 16-AUG-2001.

FT 12-FEB-2001; 2001WO-DK00094.

FT 11-FEB-2000; 2000DK-0000218.

FT 18-OCT-2000; 2000DK-0001558.

FT (MAXY-) MAXYGEN APS.

FT Andersen KV, Pedersen AH, Bornaes C;
 WPI; 2001-581807/65.

FT DR N-PSDB; AA199982.

PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -

XX PS Claim 1; Page 81-83; 89pp; English.

XX CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, cardiatic, hepatocytic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections.

XX SQ Sequence 406 AA;

Query Match 83.7%; Score 159; DB 22; Length 406;
 Best Local Similarity 95.5%; Pred. No. 1.9e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXAEXIFPDAXRTKLFWISY 44
 |||||
 Db 1 ANAFLXLRPGSLRCKXQCSFXAEXIFPDAXRTKLFWISY 44

RESULT 12

AAM52172
 ID AAM52172 standard; Protein; 406 AA.

XX AC AAM52172;

XX DT 07-FEB-2002 (first entry)

XX DE Mammalian expressed human FVII SEQ ID NO 3.

XX KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;


```

CC      (AAM52171).
XX      Sequence      406 AA;

Query Match
Best Local Similarity 83.7%; Score 159; DB 22; Length 406;
Matches 42; Conservative 95.5%; Pred. No. 1.9e-18;
                                0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44
        |||
        1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 15
AAM52183
ID      AAM52183 Standard; Protein; 406 AA.
XX
AC      AAM52183;
XX
DT      07-FEB-2002 (first entry)
XX
DE      Human FVII mutant V253N.
XX
XX      Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM      cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KM      myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KM      mutain.
XX
XX      Homo sapiens.
OS
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 6 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 7 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 14 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 16 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 19 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 20 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 25 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 26 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 29 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 35 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Modified-site 52 /note= "O-glycosylated"
FT      Modified-site 60 /note= "O-glycosylated"
FT      Modified-site 145 /note= "N-glycosylated"
FT      Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Misc-difference 253

```

```

FT      /note= "wild-type Val substituted by Asn"
FT      Modified-site 322 /note= "N-glycosylated"
FT
XX      WO200158935-A2.
XX
XX      16-AUG-2001.
XX
XX      12-FEB-2001; 2001WO-DK00094.
XX
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX
XX      (MAXY-) MAXYGEN APS.
XX
XX      Andersen KV, Pedersen AH, Bornaes C,
XX      WPI; 2001-581807/65.
XX
XX      New conjugate, useful for treating Factor VIIa related diseases or
PT      disorders such as haemophilia, liver disease, myocardial infarction and
PT      deep-vein thrombosis, comprises non-polypeptide group covalently
PT      attached to polypeptide group -
XX
XX      Example 3; Page -: 89pp; English.
XX
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC      polypeptide conjugates, comprising at least one non-polypeptide group
CC      covalently attached to a polypeptide, where the amino acid sequence of
CC      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC      least one amino acid residue containing an attachment group for the
CC      non-polypeptide group has been introduced or removed. The FVIIa
CC      conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
CC      cerebroprotective activity and are useful for treating FVIIa/TF-related
CC      diseases or disorders such as haemophilia, liver disease, myocardial
CC      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC      have increased functional in vivo half life and/or increased plasma half
CC      life, increased bioavailability and/or reduced sensitivity to proteolytic
CC      degradation. Consequently medical treatment using the conjugates has a
CC      number of advantages over currently available such as longer duration
CC      between injections. The present sequence is that of a human FVII mutant,
CC      having an addition in vivo glycosylation site and tested for its
CC      amidolytic activity.
CC      Note: The present sequence is not shown in the specification but is
CC      derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC      (AAM52171).
XX
XX      Sequence      406 AA;
SQ

Query Match
Best Local Similarity 83.7%; Score 159; DB 22; Length 406;
Matches 42; Conservative 95.5%; Pred. No. 1.9e-18;
                                0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44
        |||
        1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

DB      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

```

Search completed: March 19, 2003, 14:51:07
Job time : 32.4375 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28GLU

Perfect score: 190

Sequence: 1 ANAFLLXDLREGSLXRXCKX.....XXAEXIFMDAXRTKLFWISY 44

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	466	1 KFHU7	coagulation factor
2	125	65.8	443	2 I46932	coagulation factor
3	115	60.5	407	1 KFB07	coagulation factor
4	102	53.7	461	1 JX0210	protein C (activat
5	101	53.2	461	1 S18994	protein C (activat
6	99	52.1	488	1 EXHU	coagulation factor
7	99	52.1	492	1 EXBO	coagulation factor
8	93	48.9	482	1 EXRT	coagulation factor
9	91	47.9	456	1 KXBO	protein C (activat
10	89	46.8	475	1 EXCH	coagulation factor
11	85	44.7	462	1 KXHU	protein C (activat
12	85	44.7	621	1 TBHU	thrombin (EC 3.4.2
13	81	42.6	416	1 KFB0	coagulation factor
14	81	42.6	617	2 S10511	thrombin (EC 3.4.2
15	81	42.6	618	2 A35827	thrombin (EC 3.4.2
16	80	41.1	461	1 KFHU	coagulation factor
17	73	38.4	452	1 A30351	coagulation factor
18	73	38.4	459	2 J00419	coagulation factor
19	67	35.3	642	2 S53433	coagulation factor
20	65	34.2	625	1 TBBO	plasma protein S p
21	64	33.7	396	1 KXBOZ	plasma protein Z -
22	63	33.2	675	1 KXBOS	plasma protein S p
23	62	32.6	642	2 S53434	plasma protein S p
24	62	32.6	676	1 KKHUS	plasma protein S p
25	61	32.1	646	2 S38819	plasma protein S -
26	60	31.6	675	1 KXRTS	plasma protein S p
27	59	31.1	422	1 KXHUZ	plasma protein Z p
28	58.5	30.8	576	2 G96763	probable MAP kinase
29	53	27.9	673	2 A48089	growth arrest-spec

30	53	27.9	675	1 KXMS	plasma protein S p
31	52.5	27.6	594	2 D84859	probable MAP kinase
32	52.5	27.6	603	2 C96575	probable MAP kinase
33	51	26.8	674	2 I55476	growth potentialin
34	51	26.8	678	2 B88089	growth potentialin
35	48.5	25.5	455	2 C83494	growth arrest-spec
36	48	25.3	211	2 D66996	uncharacterized lo
37	45	23.7	879	2 S55864	uncharacterized prote
38	44	23.2	413	1 VHVNIH	hypothetical prote
39	44	23.2	447	2 B95185	nucleoprotein - in
40	44	23.2	447	2 B88052	Mur ligase family
41	43.5	22.9	322	2 T20272	conserved hypotnet
42	42.5	22.4	161	2 F82637	hypothetical prote
43	42.5	22.4	319	2 T15137	conserved hypotnet
44	42.5	22.4	410	2 T25574	hypothetical prote
45	42.5	22.4	907	2 T15792	hypothetical prote

ALIGNMENTS

RESULT 1

KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A28319; A3186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.V.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:G180333; PIDN:AAA51883.1; PID:G180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A>Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A28319; MUID:86205965; PMID:3466420
A:Accession: A28319
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M3232; NID:G182799; PIDN:AAA8040.1; PID:G182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wilberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A>Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A:Reference number: A40529; MUID:91250411; PMID:1904059
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; MUID:96096752; PMID:8525655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <Gla>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:177-82,110-121,115-130,139-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:1203/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carboxylate (Asn) (covalent) #status experimental
F:112-213/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
F:253,302,404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1,9e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXKCKXKQCFXAXEYFKDAXRTKLFMISY 44
DB 61 ANAFLEELRPGSLERBECKEELCFEEAHEIFKDEKRTKLFMISY 104

RESULT 2
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: 146932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: 146932; MUID:93190306; PMID:8393365
A:Accession: 146932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1443 <PRO>
A:Cross-references: GB:S56300, NID:g266294, PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <Gla>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 65.8%; Score 125; DB 2; Length 443;
Best Local Similarity 54.5%; Pred. No. 1,4e-13;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXKCKXKQCFXAXEYFKDAXRTKLFMISY 44
DB 40 ANAFLEELRPGSLERBECKEELCFEEAHEIFKDEKRTKLFMISY 83

RESULT 3
KFB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; MUID:89008362; PMID:3049594
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCM>
A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R:Nase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Suyoshi, T.; Miyata, T.; Iwanaga, U. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX
A:Reference number: A44556; MUID:89213999; PMID:3149637
A:Contents: annotation
A>Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:1-44/Domain: Gla domain homology (fragment) <Gla>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/
F:52/Binding site: carboxylate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental
F:152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 60.5%; Score 115; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 6,9e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXKCKXKQCFXAXEYFKDAXRTKLFMISY 44
DB 1 ANAFLEELRPGSLERBECKEELCFEEAHEIFRNEERTKPFWSY 44

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: Vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that is

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:34-41/Domain: propeptide #status predicted <PRO>
F:47-196,199-461/Product: protein C #status predicted <PC>
F:44-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

J. Mol. Biol. 232, 947-966, 1993

A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.

A/Reference number: A49458; PMID:93360277; PMID:8355219

A/Contents: annotation; X-ray crystallography, 2.2 angstroms

C/Comment: The two chains held together by one disulfide bond are formed from a single-c

C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or

C/Genetic: GDB:P10

A/Cross-references: GDB:119890; OMIM:227600

A/Map position: 13q34-13q34

A/Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1

A/Note: Efficiency of this factor causes Stuart disease

C/Function: Defect

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-40/Domain: propeptide #status predicted <PRO>

F/25-84/Domain: Gla domain homology <Gla>

F/41-179/Product: coagulation factor X light chain #status experimental <LCH>

F/90-121/Domain: EGF homology <EGF>

F/129-164/Domain: EGF homology <EG2>

F/183-488/Product: coagulation peptide #status experimental <APT>

F/235-234/Domain: activation peptide #status experimental <ACT>

F/335-462/Domain: trypsin homology <TRY>

F/46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F/57-62/Diulfide bonds: #status predicted

F/80-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/

F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F/129,211/Binding site: carboxylate (Thr) (covalent) #status experimental

F/221,231/Binding site: carboxylate (Asn) (covalent) #status experimental

F/234-235/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat

F/276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 52.1%; Score 99; DB 1; Length 488;

Best Local Similarity 38.6%; Pred. NO. 4.8e-09;

Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFXXLRGSLRXCKXXCSEFXAEXIFKDXARTLFWISY 44

41 ANSLFEMKKGHLEKMEETCSYEBAREVEDSDKTNEFNKKY 84

Db

RESULT 7

EXBO

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N/Alternate names: Stuart factor

C/Species: Bos primigenius taurus (cattle)

C/Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text change 16-Jul-1999

C/Accession: A22867; A14997; A12030; A34412; S39414; A00925

R/Pung: M.R.; Campbell, R.M.; MacGillivray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a

A/Reference number: A22867; PMID:84247315; PMID:6330671

A/Accession: A22867

A/Molecule type: mRNA

A/Residues: 1-487 <FNU>

A/Cross-references: GB:X00673; NID:q192; PIDN:CA28286.1; PID:q193

R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.

Biochemistry 19, 659-667, 1980

A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).

A/Reference number: A14997; PMID:80130563; PMID:6766735

A/Accession: A14997

A/Molecule type: protein

A/Residues: 41-102, 'N', 104-180 <ENP>

R/McMullen, B.A.; Fujikawa, K.; Kiesel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood ec

A/Reference number: A20274; PMID:83308813; PMID:6688526

A/Contents: annotation; revision to residue 103

R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975

A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

A/Reference number: A12030; PMID:76053069; PMID:1059993

A/Accession: A12030

A/Molecule type: protein

A/Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T

A/Note: carboxylate binding sites and disulfide bonds were determined

R/Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.

J. Biol. Chem. 264, 16897-16904, 1989

A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal

A/Reference number: A34412; PMID:89380326; PMID:2789221

A/Accession: A34412

A/Molecule type: protein

A/Residues: 85-126 <PER>

R/Imoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A/Reference number: S39414; PMID:94062825; PMID:8243461

A/Accession: S39414

A/Molecule type: protein

A/Residues: 183-196,199-209,216-233 <IND>

A/Note: carboxylate binding sites

R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D

Biochemistry 11, 4899-4903, 1972

A>Title: Bovine factor X-1a (activated Stuart factor): Evidence of homology with mammali

A/Reference number: A12453; PMID:73053314; PMID:4264286

A/Contents: annotation; active site

R/Fujikawa, K.; Titani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975

A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to

A/Reference number: A13504; PMID:76053121; PMID:1059122

A/Contents: annotation; activation

R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

J. Biol. Chem. 259, 5705-5710, 1984

A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic

A/Reference number: A38024; PMID:84185716; PMID:6546930

A/Contents: annotation; calcium binding

R/Morita, T.; Jackson, C.M.

J. Biol. Chem. 261, 4008-4014, 1986

A/Reference number: A38025; PMID:86140210; PMID:3949800

A/Contents: annotation; sulfide binding

C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.

C/Comment: The two chains are formed from a single-chain precursor by the excision of tw

C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o

activation.

C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C/Genetic:

A/Genes: P10

A/Map position: 13q34

C/Function: Defect

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-40/Domain: propeptide #status predicted <PRO>

F/41-180/Product: coagulation factor X light chain #status experimental <LCH>

F/90-121/Domain: EGF homology <EG1>

F/129-164/Domain: EGF homology <EG2>

F/183-492/Product: coagulation factor X heavy chain #status experimental <HCH>

F/183-233/Domain: activation peptide #status experimental <APT>

F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F/234-461/Domain: trypsin homology <TRY>

F/46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s

F/57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/disulfide bonds: #status p

F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F/200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F/208,485/Binding site: carboxylate (Thr) (covalent) #status experimental

F/218/Binding site: carboxylate (Asn) (covalent) #status experimental

F/233-234/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat

F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 52.1%; Score 99; DB 1; Length 492;
Best Local Similarity 40.9%; Pred. No. 4,9e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXRGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
Db 41 ANSFLEEVKQGNLERECLEACSLSEARVFEPAEDQTFDEWMSKY 84

RESULT 8

EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #ext_change 08-Dec-2000

C:Accession: S49075; J04670; P0191; P0190; 162745

R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995

A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra
A:Reference number: A58498; MUID:96093366; PMID:8578539

A:Accession: S49075

A:Molecule type: mRNA

A:Residues: 1-482 <STAI>

A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601

A>Note: submitted to the EMBL Data Library, June 1994

A>Note: neither the complete nucleic acid sequence nor the complete translation are show
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996

A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: J04670; MUID:96194815; PMID:8647460

A:Accession: J04670

A:Molecule type: mRNA

A:Residues: 1-482 <STAC>

A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601

A:Experimental source: Cos-1 cell

R:Enlyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991

A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
A:Reference number: P0190; MUID:92041742; PMID:1718949

A:Accession: P0191

A:Molecule type: protein

A:Residues: 41-58 'X', 60-65 <ENJ1>

A:Accession: P0190

A:Molecule type: protein

A:Residues: 183-186 'X', 188-207 <ENJ2>

R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994

A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A:Reference number: I46196; MUID:94222160; PMID:8168596

A:Accession: I62745

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 295-383 'G', 385-455 <MUR>

A:Cross-references: GB:D12125; NID:9415309; PIDN:BA04756.1; PID:9455396

C:Function:

A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F:1-23/Domain: signal sequence #status predicted <SIG>

F:124-40/Domain: propeptide #status predicted <PRO>

F:15-84/Domain: Gla domain homology <GLA>

F:41-179/Product: coagulation factor X light chain #status predicted <LCH>

F:90-121/Domain: EGF homology <EGF>

F:129-164/Domain: EGF homology <EG2>

F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>

F:183-231/Domain: activation peptide #status predicted <APT>

F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>

F:232-460/Domain: trypsin homology <TRY>

F:56-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat

F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat
F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.9%; Score 93; DB 1; Length 482;
Best Local Similarity 38.6%; Pred. No. 5.2e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXRGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
Db 41 ANSFPEIKKQGNLERECVEICSFEEARVFEEDNKTETFMNXY 84

RESULT 9

KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoprothrombin IIA; plasma protein C

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #ext_change 16-Jul-1999

C:Accession: A26250; A18385; A18386; A00928

R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250

A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385

A:Molecule type: protein

A:Residues: 40-194 <FER>

A>Note: 82-Lys was also found

R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939

A:Contents: annotation; revision to residue 110

R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386

A:Molecule type: protein

A:Residues: 197-454 'PV' <STB>

R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxylglutamic acid-domainless p
A:Reference number: A37541; MUID:8313513; PMID:6304092

A:Contents: annotation; activation; calcium binding

R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A:Reference number: A37542; MUID:8313514; PMID:6406503

A:Contents: annotation; activation; calcium binding

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

B:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti

C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stro

C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-23/Domain: signal sequence (fragment) #status predicted <SIG>

F:24-93/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

Q1 ANAF1XLRGSLRXCKXXCQSFYXAEKIFDARNTLFWISY 44

Db 41 ANSPLEMKQGNIERCNEBRCSEKREARFAEDNKEETEEFNWY 84

RESULT 11

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human

N.Alternate names: autoprothrombin IIA; plasma protein C

C.Species: Homo sapiens (man)

C.Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999

C.Accession: A22331; A25426; A21781; A23789; A00927

R.Fosterer, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A.Title: The nucleotide sequence of the gene for human protein C.

A.Reference number: A22331; MUID:85270390; PMID:2991887

A.Accession: A22331

A.Molecule type: DNA

A.Residues: 1-461 <FOS3>

A.Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334

R.Plutsky, J., Hosking, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 346-350, 1986

A.Title: Evolution and organization of the human protein C gene.

A.Reference number: A25426; MUID:86120978; PMID:3511471

A.Accession: A25426

A.Molecule type: DNA

A.Residues: 1-445, 'L', 446-461 <PLU>

A.Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332

R.Fosterer, D.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A.Title: Characterization of a cDNA coding for human protein C.

A.Reference number: A21781; MUID:84272714; PMID:6589623

A.Accession: A21781

A.Molecule type: mRNA

A.Residues: 'Q', 107-461 <FOS2>

A.Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323

R.Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L

Nucleic Acids Res. 13, 5233-5247, 1985

A.Title: The structure and evolution of a 461 amino acid human protein C precursor and

A.Reference number: A23789; MUID:85269639; PMID:2991859

A.Accession: A23789

A.Molecule type: mRNA

A.Residues: 1-461 <BEC>

A.Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120

R.Milietich, J.P.; Broeze Jr., G.J.

J. Biol. Chem. 265, 11397-11404, 1990

A.Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation

A.Reference number: A44606; MUID:90293094; PMID:1694179

A.Contents: annotation; carbohydrate binding sites; activation peptide

A.Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not

R.Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A.Title: O-linked fucose is present in the first epidermal growth factor domain of factor

A.Reference number: A44606; MUID:92184750; PMID:1544894

A.Contents: annotation; beta-hydroxyaspartic acid

A.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that ir

A.Comment: factor Va is strongly enhanced by complexing with protein S. Protein C also f

A.Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,

C.Genetics:

A.Gene: GDB:PROC

A.Cross-references: GDB:120317; OMIM:176860

A.Map position: 2q13-q21

A.Intron: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C.Specificity: coagulant; factor X; EGF homology; Gla domain homology; trypsin homology

C.Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F.1-37/Domain: signal sequence #status predicted <SIG>

F.27-86/Domain: Gla domain homology <Gla>

F.33-42/Domain: propeptide #status predicted <PRO>

F.43-197/Domain: EGF homology <EGF>

F.92-131/Domain: protein C light chain #status predicted <LCH>

F.140-175/Domain: EGF homology <EG2>

F.200-461/Domain: protein C heavy chain #status predicted <HCH>

F.200-211/Domain: activation peptide #status experimental <AP>

F.212-445/Domain: trypsin homology <TRY>
 F.48, 49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F.59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/D
 F.106-111/Disulfide bonds: #status predicted
 F.110/Binding site: carboxylate (Thr) (covalent) #status absent
 F.113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F.139, 299, 355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F.211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F.253, 299, 402/Active site: His, Asp, Ser #status predicted
 F.371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 44.7%; Score 85; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 1.2e-06;
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXQCSFXAEXIFPDAXTKLFW 41
 DB 43 ANSFLERHRSILRECEIERICDFEAKELFQVNDTLAEW 83

RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human
 N:Alternate names: coagulation factor II
 N:Contains: prothrombin
 C:Species: Homo sapiens (man)
 C>Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #ext change 08-Dec-2000
 C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
 R:Degein, S.J.F.; Davie, E.W.
 Biochemistry 26, 6165-6177, 1987
 A>Title: Nucleotide sequence of the gene for human prothrombin.
 A:Reference number: A29351; PMID:88077877; PMID:2825773
 A:Accession: A29351

A:Molecule type: DNA
 A:Residues: 1-622 <DEG>
 A:Cross-references: GB:M17262; GB:M33691; NID:9558069; PIDN:AC63054.1; PID:G339641
 R:Degein, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
 Biochemistry 22, 2087-2097, 1983
 A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
 A:Reference number: A00914; PMID:83231469; PMID:6305407
 A:Accession: A00914

A:Molecule type: mRNA
 A:Residues: 8-163, 'N', 165-622 <DE2>
 A:Cross-references: GB:V00595; GB:J00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344
 A:Accession: B00914

A:Molecule type: DNA
 A:Residues: 188-311 <DE3>
 R:Walt, D.A.; Hewett-Emmett, D.; Seeger, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
 A:Reference number: A37549; PMID:77193964; PMID:266717
 A:Accession: A37549

A:Molecule type: protein
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'WV', 196-308,
 R:Butkowski, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.
 J. Biol. Chem. 252, 4942-4957, 1977
 A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.
 A:Reference number: A37550; PMID:77207112; PMID:873923
 A:Accession: A37550

A:Molecule type: protein
 A:Residues: 315-334, 'N', 336-348, 'N', 350-366, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 J:Rabiet, M.J.; Blachill, A.; Furie, B.; Furie, B.C.
 J. Biol. Chem. 261, 13310-13315, 1986
 A:Reference number: A37551; PMID:87008532; PMID:3759958
 A:Contents: annotation; activation cleavages
 R:MacGillivray, R.T.; Irwin, D.M.; Guinno, E.R.; Stone, J.C.
 Ann. N.Y. Acad. Sci. 485, 73-79, 1986
 A>Title: Recombinant genetic approaches to functional mapping of thrombin.
 A:Reference number: I51952; PMID:87182874; PMID:3471151
 A:Accession: I51952

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2, 'RI', 5-100 <RES>
 A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
 C/Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
 C/Comment: can be removed either by factor Xa or thrombin: the cleavage into light and heavy chain
 ter 314-Arg, are released in natural blood clotting.
 C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
 C/Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
 ent interaction with the negatively charged phospholipid membrane surface.
 C/Comment: The prothrombin precursor is synthesized in the liver.
 C:Genetic8:

A:Gene: GDB:F2
 A:Cross-references: GDB:119894; OMIM:176930

A:Map position: 11p11-11q12
 A:Insertions: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
 C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli

F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-43/Domain: propeptide #status predicted <PRO>
 F.28-87/Domain: Gla domain homology <Gla>
 F.44-622/Product: prothrombin #status experimental <MAT>
 F.44-327/Domain: activation peptide #status experimental <APT>
 F.108-186/Domain: kringe homology <KR1>
 F.213-291/Domain: kringe homology <KR2>
 F.328-363/Domain: thrombin light chain #status experimental <LCH>
 F.364-622/Product: thrombin heavy chain #status experimental <HCH>
 F.364-613/Domain: trypsin homology <TRY>
 F.49, 50, 57, 59, 62, 63, 68, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F.60-65, 90-103, 108-186, 129-159, 157-181, 213-291, 234-274, 262-286/Disulfide bonds: #status
 F.221, 143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F.336-482, 536-550, 564-594/Disulfide bonds: #status predicted
 F.391-407/Disulfide bonds: #status experimental
 F.406, 462/Active site: His, Asp #status predicted
 F.416/Binding site: carboxylate (Asn) (covalent) #status experimental
 F.568/Active site: Ser #status experimental

Query Match 44.7%; Score 85; DB 1; Length 622;
 Best Local Similarity 36.4%; Pred. No. 1.6e-06;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXQCSFXAEXIFPDAXTKLFWISY 44
 DB 44 ANTFLEVRKGNLRECEVETCSYEAPALBSTATDVFWAKY 87

RESULT 13

KEBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N:Alternate names: Christmas factor
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #ext change 16-Jul-1999
 C:Accession: A14757; B20274; I45891; A00923
 R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
 A>Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
 A:Reference number: A14757; PMID:80056619; PMID:291916
 A:Accession: A14757

A:Molecule type: protein
 A:Residues: 1-63, 'T', 65-416 <KAT>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; PMID:83308813; PMID:6688526
 A:Accession: B20274

A:Molecule type: protein
 A:Residues: 59-63, 'X', 65-69 <MCW>
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A>Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
 A:Reference number: I45891; PMID:82272386; PMID:6287289
 A:Accession: I45891

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 52-139 <CHO>
 A:Cross-references: GB:J00007; NID:G163053; PIDN:AAA30520.1; PID:G163054

R.Hase, S.; Kawabara, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, U. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag A:Reference number: A44556; PMID:89213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of a carbohydrate covalently bound to Ser C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pres A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F:1-16/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <GLA>
F:51-82/Domain: EGF homology <EG1>
F:88-124/Domain: EGF homology <EG2>
F:147-181/Product: activation peptide #status experimental <APT>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta F:18-23,51-62,56-71,73-82,88-99,95-111,124,132-290,207-223,337-351,362-390/Dismulfide F:53/Binding site: carboxylate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 42.6%; Score 81; DB 1; Length 416;
Best Local Similarity 41.2%; Pred. No. 5,4e-06;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLLRXCKXXQCSFXAXEYFKDAXRTKLFWISY 44
Db 12 GNLEKCKEKCSFEAREVFEKTEKTEPMKQY 45

RESULT 14

S10511
thrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C:Accession: S10511; A60576; B26896
R:Banfield, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
A:Reference number: S10511; PMID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DIH>
A:Cross-references: EMBL:X52835; NID:G5669; PIDN:CAA37017.1; PID:G56970
R:Henriksson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A:Reference number: A60576; PMID:90091942; PMID:12293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A:Reference number: A42696; PMID:92212913; PMID:1557383
A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr F:25-43/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:29-86/Domain: Gla domain homology <GLA>

F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringe homology <KR1>
F:215-292/Domain: kringe homology <KR2>
F:260-609/Domain: trypsin homology <TRY>
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F:51-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5 F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 42.6%; Score 81; DB 2; Length 617;
Best Local Similarity 37.2%; Pred. No. 7,9e-06;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

OY 2 NAFLLXLRGSLRXCKXQCSFXAXEYFKDAXRTKLFWISY 44
Db 46 SGFLLELRKGNLRECVCEGCSYFEAFEALESQDDIVFMAKY 88

RESULT 15

A35827
thrombin (EC 3.4.21.5) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 03-May-2002
C:Accession: A35827; A42696; S12081
R:Deegen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.U.; Pai, J.A. DNA Cell Biol. 9, 487-498, 1990
A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of t A:Reference number: A35827; PMID:91025551; PMID:2222810
A:Accession: A35827
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-618 <DEG>
A:Cross-references: GB:X52308; NID:G53813; PIDN:CAA36548.1; PID:G53814
A:Experimental source: strain C57BL/6
A:Note: the data were obtained from females resulting from the cross of M. domesticus an R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A:Reference number: A42696; PMID:92212913; PMID:1557383
A:Accession: A42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BAN>
A:Cross-references: GB:M81394
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringe homology <KR1>
F:215-293/Domain: kringe homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5 F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 42.6%; Score 81; DB 2; Length 618;
Best Local Similarity 37.2%; Pred. No. 7,9e-06;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

OY 2 NAFLLXLRGSLRXCKXQCSFXAXEYFKDAXRTKLFWISY 44
Db 46 SGFLLELRKGNLRECVCEGCSYFEAFEALESQDDIVFMAKY 88

Search completed: March 19, 2003, 15:00:46
Job time : 30.125 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLU28GLU

Sequence: 1 ANAFIXXIREGSLRXCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	466	FA7_HUMAN	P08709 homo sapien
2	125	65.8	444	FA7_RABIT	P98139 oryctolagus
3	115	60.5	407	FA7_BOVIN	P22457 bos taurus
4	114	60.0	446	FA7_MOUSE	P70375 mus musculu
5	102	53.7	461	PRTC_MOUSE	P33587 mus musculu
6	101	53.2	459	PRTC_PIG	O991p2 sus scrofa
7	101	53.2	461	PRTC_RAT	P31394 rattus norv
8	99	52.1	488	FA10_HUMAN	O19045 oryctolagus
9	99	52.1	490	FA10_RABIT	O19045 oryctolagus
10	99	52.1	492	FA10_BOVIN	O19045 oryctolagus
11	97	51.1	218	TMG1_HUMAN	O1668 homo sapien
12	91	47.9	456	PRTC_BOVIN	P00745 bos taurus
13	90	47.4	231	TMG3_HUMAN	O982d7 homo sapien
14	89	46.8	475	FA10_CHICK	P25155 gallus gall
15	85	44.7	458	PRTC_RABIT	O28661 oryctolagus
16	85	44.7	461	PRTC_HUMAN	P04070 homo sapien
17	85	44.7	622	THRB_HUMAN	P00734 homo sapien
18	81	42.6	416	FA9_BOVIN	P00741 bos taurus
19	81	42.6	617	THRB_RAT	P18292 rattus norv
20	81	42.6	618	THRB_MOUSE	P19221 mus musculu
21	80	42.1	461	FA9_HUMAN	P00740 homo sapien
22	79	41.6	376	FA10_TROCA	P81428 tropidechis
23	76	40.0	202	TMG2_HUMAN	O1669 homo sapien
24	73	38.4	452	FA9_CANFA	P15540 canis famli
25	73	38.4	459	FA9_MOUSE	P15294 mus musculu
26	69.5	36.6	226	TMG4_HUMAN	O992d6 homo sapien
27	65	34.2	625	THRB_BOVIN	P00735 bos taurus
28	64	33.7	396	PRTC_BOVIN	P00743 bos taurus
29	63	33.2	675	PRTS_BOVIN	P07224 bos taurus
30	62	32.6	649	PRTS_MACMU	O28520 macaca mula
31	62	32.6	646	PRTS_HUMAN	P98118 oryctolagus
32	61	32.1	646	PRTS_RABIT	P98118 oryctolagus
33	60	31.6	675	PRTS_RAT	P53813 rattus norv

34	59	31.1	400	PRTZ_HUMAN	P22891 homo sapien
35	53	27.9	675	PRTS_MOUSE	O08761 mus musculu
36	45	23.7	879	YN65_YEAST	P42837 saccharomyc
37	44	23.2	413	NCAP_IHNV	P19691 infectious
38	43.5	22.9	322	YOL3_CABEL	O09292 caenorhabdi
39	43	22.6	343	HMD_METVO	O50840 methanococc
40	43	22.6	353	HMD_METTL	O50759 m coenzyme
41	42	22.1	185	HEX1_MOUSE	O61658 mus musculu
42	42	22.1	263	PELA_STRMU	O68575 streptococc
43	41.5	21.8	356	MURB_BUCAI	P57153 buchemera ap
44	41.5	21.8	1290	BXB_CLOBO	P10844 clostridium
45	41	21.6	584	DWLI_AQUAE	O67398 aquifex aeo

ALIGNMENTS

RESULT 1
ID FA7_HUMAN STANDARD, PRT, 466 AA.
AC P08709; O14339;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Bplacog alfa).
CN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Riederer M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjørn S., Christensen W., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjørn S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine";
RN J. Biol. Chem. 266:11051-11057(1991).
RP [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shionomiya Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [17]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=9134709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forssen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Gasnaco A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (13His and 33Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Mellis E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chaining S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodighiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiva M., Hayashi T., Wada H., Minamikawa K., Shirekawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arhnt A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodighiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "A1244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MULTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1.4e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXKXCKXQCSFXAXEIPFDAXRTKLFWISY 44
Db 61 ANAFLXLRGSLRXKXCKXQCSFXAXEIPFDAXRTKLFWISY 104

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U77477; AAB37326.1; -
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02400; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
KM EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CMC64;

Query Match 65.8%; Score 125; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 1.5e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXKXCKXQCSFXAXEIPFDAXRTKLFWISY 44
Db 40 ANAFLXLRGSLRXKXCKXQCSFXAXEIPFDAXRTKLFWISY 83

RESULT 3

FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OK NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RT J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Klsiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RL -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to form factor Xa.
CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR PIR: A31979; A31979.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; .
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001438; EGF-TI.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00001; EGF_like_1.

DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT BINDING 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT MOD_RES 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703B1FE0636FF7F10 CRC64;
Query Match 60.5%; Score 115; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 8; 4e-13;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
CY 1 ANAFLLXLRGSLXRCXKXQCSFXXAEXIFKDAXTKLFWISY 44
DB 1 ANGFLELLPGLSRLRCREBLCSFEAHELFNERTROFWISY 44
RESULT 4
ID FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RT Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
 BY LIMITED PROTEOLYSIS. FACTOR VIIA ALSO CONVERT FACTOR IX TO
 FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; I8P9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; glai; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 RN EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL; 1 24
 FT PROPEP; 25 41
 FT CHAIN; 42 193
 FT CHAIN; 194 446
 FT DOMAIN; 47 76
 FT DOMAIN; 87 123

FT DOMAIN 128 169 EGF-LIKE 2.
 FT DOMAIN 194 446 SERINE PROTEASE.
 FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
 FT ACT SITE 234 234 FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
 FT ACT SITE 283 283 BY SIMILARITY.
 FT ACT SITE 385 385 BY SIMILARITY.
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 113 122 BY SIMILARITY.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 139 153 BY SIMILARITY.
 FT DISULFID 155 168 BY SIMILARITY.
 FT DISULFID 176 203 BY SIMILARITY.
 FT DISULFID 200 205 BY SIMILARITY.
 FT DISULFID 219 235 BY SIMILARITY.
 FT DISULFID 351 370 BY SIMILARITY.
 FT DISULFID 381 409 BY SIMILARITY.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 446 AA; 50276 MW; 2512B44A5CB966 CnC64;

Query Match 60.0%; Score 114; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 1.4e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLXKCKKXQCSFYXAXEIPKDXRTLFWISY 44
 Db 42 ANSLLEELWPSGLRECNBEOCSFEAREIFKSPRTQFWILY 85

RESULT 5
 PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Antiproteohormin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 "Isolation and characterization of a mouse protein C cDNA."
 RL J. Biochem. 111:491-495(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=96152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 "Nucleotide structure and characterization of the murine gene encoding

```

RT  anticoagulant protein C."
RU  Thromb. Haemost. 79:310-316(1998).
RN  [3]
RP  SEQUENCE OF 274-434 FROM N.A.
RC  STRAIN=BALB/c;
RX  MEDLINE=94318474; PubMed=8043441;
RA  Murkawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT  "A comparative study of partial primary structures of the catalytic
RT  region of mammalian protein C."
RL  Br. J. Haematol. 86:590-600(1994).
CC  -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC  REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC  IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC  -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC  and VIIIA.
CC  -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC  INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC  BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC  TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC  REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC  STRONGLY PROMOTED BY THROMBOMODULIN.
CC  -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC  -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC  GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC  -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC  ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC  SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC  THROMBIN-THROMBOMODULIN COMPLEX.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC  -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-----
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CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL, D10445; BAA01235.1; -.
DR  EMBL, AF034569; AAC3795.1; -.
DR  EMBL, D43755; BAA07812.1; -.
DR  PIR, JX0210; JX0210.
DR  HSSP, P04070; JPCU.
DR  MEROPS, S01.218; -.
DR  MGD, MGI:97771; Proc.
DR  InterPro, IPR000152; Asx_hydroxyl.
DR  InterPro, IPR001314; Chymotrypsin.
DR  InterPro, IPR000561; EGF-like.
DR  InterPro, IPR001881; EGF Ca.
DR  InterPro, IPR002383; GLA_blood.
DR  InterPro, IPR001254; Ser_protease_Try.
DR  InterPro, IPR000294; VitK_dep_GLA.
DR  Pfam, PF00008; EGF_2.
DR  Pfam, PF00089; trypsin; 1.
DR  Pfam, PF00594; gla; 1.
DR  PRINTS, PRO0722; CHYMOTRYPSIN.
DR  PRINTS, PRO0001; GLABLOOD.
DR  SMART, SM00179; EGF CA; 1.
DR  SMART, SM00001; EGF_like; 1.
DR  SMART, SM00069; GLA; 1.
DR  SMART, SM00020; Tryp_SPC; 1.
DR  PROSITE, PS00010; ASX_HYDROXYL; 1.
DR  PROSITE, PS00022; EGF_1; 1.
DR  PROSITE, PS01186; EGF_2; 2.
DR  PROSITE, PS01187; EGF CA; 1.
DR  PROSITE, PS00011; GLU CARBOXYLATION; 1.
DR  PROSITE, PS00240; TRYPSIN_DOM; 1.
DR  PROSITE, PS00134; TRYPSIN_HIS; 1.
DR  PROSITE, PS00135; TRYPSIN_SER; 1.
DR  Blood coagulation; Glycoprotein; Serine protease;
KW  Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW  EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

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FT  SIGNAL 1 33
FT  PROPER 34 41
FT  CHAIN 42 196
FT  CHAIN 199 461
FT  PEPTIDE 199 212
FT  SITE 212 213
FT  DOMAIN 96 131
FT  DOMAIN 135 175
FT  DOMAIN 213 461
FT  MOD_RES 47 47
FT  MOD_RES 48 48
FT  MOD_RES 55 55
FT  MOD_RES 57 57
FT  MOD_RES 60 60
FT  MOD_RES 61 61
FT  MOD_RES 66 66
FT  MOD_RES 67 67
FT  MOD_RES 70 70
FT  MOD_RES 70 70
FT  MOD_RES 112 112
FT  ACT_SITE 253 253
FT  ACT_SITE 299 299
FT  ACT_SITE 402 402
FT  DISULFID 58 63
FT  DISULFID 91 110
FT  DISULFID 100 105
FT  DISULFID 104 119
FT  DISULFID 121 130
FT  DISULFID 139 150
FT  DISULFID 146 159
FT  DISULFID 161 174
FT  DISULFID 182 319
FT  DISULFID 328 354
FT  DISULFID 373 387
FT  DISULFID 398 426
FT  CARBOHYD 214 214
FT  CARBOHYD 290 290
FT  CARBOHYD 355 355
FT  CARBOHYD 328 328
FT  CONFLICT 393 393
SQ  SEQUENCE 461 AA; 51945 MW; 53FA0D85B194D6E CRC64;

Query Match 53.7%; Score 102; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 2e-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFDXATKTLFWISY 44
DB 42 ANSFLEMRPGSLRRCMBECIDFERRQELFQVVEDTLAFWIKY 85

RESULT 6
PRIC_PIG STANDARD; PRT; 459 AA.
AC 09GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae; Suidae.

```

OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter W.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the Gla domain. This Gla-independent binding
CC site is necessary for the recognition of the
CC thrombin-thrombomodulin complex.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC DR EMBL; AF191307; AAG28380.1; -;
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -;
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; Gla blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_Gla.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF-like; 2.
DR SMART; SM00069; Gla; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF-Ca; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 18
FT PROPEP 19 41 BY SIMILARITY.
FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.

FT	CHAIN	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199	459	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199	213	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	213	214	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	214	459	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	255	255	CHARGE RELAY SYSTEM.
FT	ACT_SITE	301	301	CHARGE RELAY SYSTEM.
FT	ACT_SITE	400	400	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	321	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	240	256	BY SIMILARITY.
FT	DISULFID	371	385	BY SIMILARITY.
FT	DISULFID	396	424	BY SIMILARITY.
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	459 AA;	51866 MW;	8541AAC14CCL16D09 CRC64;

Query Match 53.2%; Score 101; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 3e-10; Indels 0; Gaps 0;
Matches 20; Conservative 3; Mismatches 21;

QY 1 ANAFLLXLRREGSLXRXCKXCCFFXXAEXIFDARRTKLFWSY 44
DB 42 ANSFLELRPSLRRECKEFTCDFEARRIFONTENTMAFNKSY 85

RESULT 7
PRTC_RAT STANDARD; PRT; 461 AA.
AC P31354;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIR) (Anticoagulant protein C) (Blood coagulation factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okatsuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.;"
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADSCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X64336; CAA45617.1; -.
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSP; P04070; IPCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001861; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLUTCARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Blood coagulation: Glycoprotein; Serine protease;
KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 32
FT PROPEP 33 41 BY SIMILARITY.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).

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FT SITE 212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 213 461 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 47 47 (BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 48 48 (BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 254 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;

Query Match 53.2%; Score 101; DB 1; Length 461;
Best Local Similarity 45.5%; Pred No. 36-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXRTKLFWISY 44
Db 42 ANSFLEVRAGSLERECMEICDFEEAQEIFQVEDTLAFWIKY 85

RESULT 8
FA10 HUMAN STANDARD; PRT; 488 AA.
ID FA10 HUMAN 014340:
AC P00752; O14340:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RL human coagulation factor X.;"
RN Gene 99:291-294 (1991).

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RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768335;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN (3)
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN (4)
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN (5)
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistel W., Sasegawa T., Howald W.N.,
 RA Kwa B.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN (6)
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN (7)
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (8)
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=9012829; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusnam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN (9)
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blumenship D.T., Garoin A.D., Kistel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN (10)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Homma T., Iwana T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; K03194; AAA52490.1; -
 DR EMBL; M57285; AAA52421.1; -
 DR EMBL; L29433; AAA52764.1; -
 DR EMBL; L00390; AAA52764.1; JOINED.
 DR EMBL; L00391; AAA52764.1; JOINED.
 DR EMBL; L00392; AAA52764.1; JOINED.
 DR EMBL; L00393; AAA52764.1; JOINED.
 DR EMBL; L00394; AAA52764.1; JOINED.
 DR EMBL; L00395; AAA52764.1; JOINED.
 DR EMBL; L00396; AAA52764.1; JOINED.
 DR EMBL; M22613; AAA51984.1; -
 DR EMBL; K01886; AAA52486.1; -
 DR EMBL; M33297; AAA52636.1; -
 DR PIR; A00924; EXHU
 DR PIR; A05853; A25853.
 DR PIR; A24478; A24478.
 DR PDB; 1HCG; 08-MAY-95.
 DR PDB; 1FAX; 29-OCT-97.
 DR PDB; 1EXY; 17-JUN-98.
 DR PDB; 1XKA; 23-MAR-99.
 DR PDB; 1XKB; 23-MAR-99.
 DR MEROPS; S01.216; -
 DR GlycoSuiteDB; P00742; -
 DR GeneW; HGNC:3528; F10.
 DR MIM; 134530; -
 DR MIM; 227600; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRY_P; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF 2; 1.
 DR PROSITE; PS01186; EGF 2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00340; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

CC		GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC		CALCIUM (BY SIMILARITY).
CC	-1-	PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC	-1-	PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY) (BY SIMILARITY).
CC	-1-	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC	-1-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	-1-	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as their content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcement/or_send_an_email_to_license@ebi.ac.uk).
CC		-----
DR	EMBL; AF003200; AAB62542.1; -	
DR	HSSP; P00742; IHCG.	
DR	MEROPE; S01.216; -	
DR	InterPro; IPR000152; Aex_hydroxyl.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR00742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR002383; GLA_Blood.	
DR	InterPro; IPR001254; Ser_protease_Try.	
DR	InterPro; IPR000294; VitK_dep_GLA.	
DR	Pfam; PF00008; EGF_2.	
DR	Pfam; PF00089; trypsin; 1.	
DR	Pfam; PF00594; gla; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	SMART; SM00179; EGF_Ca; 1.	
DR	SMART; SM00001; EGF_like; 1.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00020; Tryp_spec; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; Glu_CARBOXYLATION; 1.	
DR	PROSITE; PS050240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KW	Glycoprotein, Hydrolase, Serine protease, Plasma, Blood coagulation, Gamma-carboxyglutamic acid, Hydroxylation, Calcium-binding, Vitamin K,	
KV	Signal; Zymogen; EGF-like domain; Repeat.	
FT	SIGNAL	1 20 POTENTIAL.
FT	PROPEP	21 40 BY SIMILARITY.
FT	CHAIN	41 180 FACTOR X LIGHT CHAIN.
FT	CHAIN	184 490 FACTOR X HEAVY CHAIN.
FT	PROPEP	184 232 ACTIVATION PEPTIDE.
FT	CHAIN	233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	DOMAIN	86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	125 165 EGF-LIKE 2.
FT	MOD_RES	233 490 SERINE PROTEASE.
FT	MOD_RES	46 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).


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FT  MOD_RES      66      66      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      69      69      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      72      72      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      75      75      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      79      79      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      103     103     HYDROXYLATION (BY SIMILARITY).
FT  ACT_SITE     274     274     CHARGE RELAY SYSTEM.
FT  ACT_SITE     320     320     CHARGE RELAY SYSTEM.
FT  ACT_SITE     417     417     CHARGE RELAY SYSTEM.
FT  DISULFID     90      101     BY SIMILARITY.
FT  DISULFID     95      110     BY SIMILARITY.
FT  DISULFID     112     121     BY SIMILARITY.
FT  DISULFID     129     140     BY SIMILARITY.
FT  DISULFID     136     149     BY SIMILARITY.
FT  DISULFID     151     164     BY SIMILARITY.
FT  DISULFID     172     240     INTERCHAIN (BY SIMILARITY).
FT  DISULFID     239     244     BY SIMILARITY.
FT  DISULFID     259     275     BY SIMILARITY.
FT  DISULFID     388     402     BY SIMILARITY.
FT  DISULFID     413     441     BY SIMILARITY.
FT  CARBOHYD     61      61      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     187     187     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     205     205     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE      490 AA; 53965 MM; 3A35FA85AF2A6D11 CR664;

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Query Match      52.1%; Score 99; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 7,2e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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Oy  1 ANAFLLXREGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
Db  41 ANSFLEELKGNLRECEMENCSEYEALEVFEDREKTNEFMWXY 84

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RESULT 10
ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA "Pung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RL Nucleic Acids Res. 12:4481-4492(1984).
[2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
[3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistler W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin

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RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053114; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";

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DR Pfam: PF00594; Glaf. 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA. 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83
FT TRANSMEM 84 106
FT DOMAIN 107 218
FT DOMAIN 24 61
FT DOMAIN 131 135
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AE98 CRC64;

Query Match 51.1%; Score 97; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 7.2e-10;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps

Oy 1 ANAFLLKRLREGSLRKCKKXCCSCFXKAEKXFKDKRTLEFWISY 44
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 21 ANGFEEIRQGNIRSECKEKEPCTFEAREAEAFENNEKTEKEFWSTY 64

RESULT 12
PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Antoprotrombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
ON 1
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=65014826; PubMed=60911100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
[2]
RN 2
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RL J. Biol. Chem. 257:12170-12179(1982).
[3]
RN 3
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Dikenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
[4]
RN 4
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
[5]
RN 5
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Eamon N.L., Debault L.E., Eamon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
[6]
RN 6
RP PROCESSING, AND CALCIUM-BINDING DATA.

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RA	Medline:63213514; PubMed:6406503.	
RT	"Structural changes required for activation of protein C are induced by Ca ²⁺ binding to a high affinity site that does not contain gamma-carboxyglutamic acid."	
RL	J. Biol. Chem. 258:5554-5560(1983).	
CC	-1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.	
CC	-1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.	
CC	-1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.	
CC	-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.	
CC	-1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.	
CC	-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.	
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.	
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.	
CC	-----	
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CC	-----	
DR	EMBL; K02435; AAA30685.1; -.	
DR	PIR; A00928; KXEO.	
DR	HSSP; P04070; 1PCU.	
DR	MEROPS; S01_218; -.	
DR	InterPro; IPR000152; Aex_hydroxyl.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001254; Ser_protease_Try.	
DR	InterPro; IPR000294; Vlt_dep_GLA.	
DR	Pfam; PF00008; EGF; 2.	
DR	Pfam; PF00089; trypsin; 1.	
DR	Pfam; PF00594; gla; 1.	
DR	SMART; SM00181; EGF; 2.	
DR	SMART; SM0069; GLA; 1.	
DR	SMART; SM00020; Tryp_spec; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KW	Blood coagulation; Glycoprotein; Serine protease;	
KW	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;	
KW	EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.	
FT	NON_TER	1
FT	SIGNAL	<1
FT	PROPEP	30
FT	CHAIN	40
FT	CHAIN	194
FT	PEPTIDE	197
FT	DOMAIN	94
FT	DOMAIN	133
FT	DOMAIN	211
FT	MOD_RES	45
FT	MOD_RES	46
FT	MOD_RES	53
FT	MOD_RES	53
FT	PROTEIN C LIGHT CHAIN.	
FT	PROTEIN C HEAVY CHAIN.	
FT	ACTIVATION PEPTIDE.	
FT	EGF-LIKE 1.	
FT	EGF-LIKE 2.	
FT	SERINE PROTEASE.	
FT	GAMMA-CARBOXYGLUTAMIC ACID.	
FT	GAMMA-CARBOXYGLUTAMIC ACID.	
FT	GAMMA-CARBOXYGLUTAMIC ACID.	
FT	GAMMA-CARBOXYGLUTAMIC ACID.	

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FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 110 110 HYDROXYLATION.
FT ACT_SITE 252 252 CHARGE RELAY SYSTEM.
FT ACT_SITE 298 298 CHARGE RELAY SYSTEM.
FT ACT_SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT DISULFID 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .)
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .)
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAPE683F894C209 CRC64;

Query Match 47.9%; Score 91; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.8e-08;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRXKXQCSFXAXEIPKDXRTKLFWISY 44
Db 40 ANSFLEELRPQNVRECESEVEFEAREIFQNTEDTMAFWSFY 83

RESULT 13
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RA MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF326350; AAK00955.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro; IPR002393; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT PROTEIN 3
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 79 101 POTENTIAL.
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; BA373E4848490D81 CRC64;

Query Match 47.4%; Score 90; DB 1; Length 231;
Best Local Similarity 36.4%; Pred. No. 1.4e-08;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRXKXQCSFXAXEIPKDXRTKLFWISY 44
Db 20 ANSFLEELRQGTIERECMEICSYEEVKEVFENKEXIMEFWKGY 63

RESULT 14
PALO_CHICK STANDARD; PRT; 475 AA.
AC P2515;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE (Virus activating protease) (VAP).
GN FX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorioallantoic membrane;
RA MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,
RA Ogasawara T., Nagai Y.,
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.";
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RA MEDLINE=91065352; PubMed=2174359;
RA Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hameguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.";
RL EMBO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

```

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, D00844; BAA00724.1; -
CC PIR, S15838; S15838.
CC HSP, P00742; 1HCG.
CC MEROPS, S01.216; -
CC InterPro, IPR000152; Asx_hydroxyl.
CC InterPro, IPR001314; Chymotrypsin.
CC InterPro, IPR000561; EGF-1-like.
CC InterPro, IPR000742; EGF 2.
CC InterPro, IPR001881; EGF_Ca.
CC InterPro, IPR001438; EGF_11.
CC InterPro, IPR002383; GLA_blood.
CC InterPro, IPR001254; Ser_protease_Try.
CC InterPro, IPR000294; Vtck_dep_GLA.
CC Pfam, PF00008; EGF_2.
CC Pfam, PF00594; trypsin_1.
CC PRINTS, PR00722; CHYMOTRYPSIN.
CC PRINTS, PR00010; EGFblood.
CC PRINTS, PR00001; GLABLOOD.
CC SMART, SM00179; EGF_Ca; 1.
CC SMART, SM00063; GLA; 1.
CC SMART, SM00020; TYP_Spec; 1.
CC PROSITE, PS00010; ASX_HYDROXYL; 1.
CC PROSITE, PS00022; EGF_1; 1.
CC PROSITE, PS01186; EGF_2; 2.
CC PROSITE, PS01187; EGF_Ca; 1.
CC PROSITE, PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE, PS50240; TRYPSIN_DOM; 1.
CC PROSITE, PS00134; TRYPSIN_HIS; 1.
CC PROSITE, PS00135; TRYPSIN_SER; 1.
CC GlycoProfile; Hydrolase; Serine protease; Plasma; blood coagulation;
CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
CC Signal; Zymogen; EGF-like domain; Repeat.
CC SIGNAL 1 20 OR 30, OR 31 (POTENTIAL).
CC PROPEP 21 40
CC CHAIN 41 180 FACTOR X LIGHT CHAIN.
CC CHAIN 186 475 FACTOR X HEAVY CHAIN.
CC PROPEP 186 241 ACTIVATION PEPTIDE.
CC CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
CC DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
CC DOMAIN 125 168 EGF-LIKE 2.
CC DOMAIN 241 475 SERINE PROTEASE.
CC MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).
CC MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).
CC MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).
CC MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).
CC MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).
CC MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).

FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 152 BY SIMILARITY.
FT DISULFID 154 167 BY SIMILARITY.
FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT DISULFID 247 252 BY SIMILARITY.
FT DISULFID 267 283 BY SIMILARITY.
FT DISULFID 396 410 BY SIMILARITY.
FT DISULFID 421 449 BY SIMILARITY.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 46.8%; Score 89; DB 1; Length 475;
Best Local Similarity 36.4%; Pred. No. 4.2e-08;
Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGGSLXRXCKXQCSFXXAEXIFDAXRTKLKFLWISY 44
DB 41 ANSFLEMKQGNIRECNERCSKEARAFEDNKTETEFNMIY 84

RESULT 15
ID_PRTC RABIT STANDARD; PRT; 458 AA.
AC 028661;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic cleavage) (Anticoagulant protein C) (blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen L., He X., Dahlback B.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME

CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U49933; AAA92956.1; -
CC HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_deg_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00394; gla; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 1
FT NON_TER 1
FT PROPEP 28 36 BY SIMILARITY.
FT CHAIN 37 458 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 37 192 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 195 458 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 209 210 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 91 126 EGF-LIKE 1.
FT DOMAIN 130 170 EGF-LIKE 2.
FT DOMAIN 130 458 SERINE PROTEASE.
FT MOD_RES 42 42 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 43 43 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 52 52 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 250 250 CHARGE RELAY SYSTEM.
FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.

FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
FT DISULFID 53 58 BY SIMILARITY.
FT DISULFID 86 105 BY SIMILARITY.
FT DISULFID 95 100 BY SIMILARITY.
FT DISULFID 99 114 BY SIMILARITY.
FT DISULFID 116 125 BY SIMILARITY.
FT DISULFID 134 145 BY SIMILARITY.
FT DISULFID 141 154 BY SIMILARITY.
FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MW; D75A5F990C8F29D7 CRC64;
Query Match 44.7%; Score 85; DB 1; Length 458;
Best Local Similarity 40.9%; Pred. No. 2; le-07;
Matches 18; Conservative 3; Mismatches 23; Indels 0; Gaps 0;
QY 1 ANAPLXXLRGSLXRXCKXKQCSFYXAEXIPDAXTKLFWISY 44
Db 37 ANSFLEELRPSLIERCEVECDLEBAKEIFQSVDDTLAFWYKY 80
Search completed: March 19, 2003, 14:52:46
Job time : 6.625 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFIXLRGSLKRXCKX.....XXAEXIFDAXRTKLFWISY 44

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	701	4 Q96P08	Q96P08 homo sapien
2	114	60.0	446	11 Q61I09	Q61I09 mus musculu
3	102	53.7	460	11 Q91MN8	Q91MN8 mus musculu
4	96	50.5	460	11 Q99PC6	Q99PC6 mus musculu
5	93	48.9	482	11 Q63207	Q63207 rattus norv
6	92	48.4	456	6 Q9TTR0	Q9TTR0 canis faml1
7	91	47.9	469	6 Q9GMD9	Q9GMD9 ornithorhyn
8	91	47.9	481	11 Q54740	Q54740 mus musculu
9	91	47.9	481	11 Q99L32	Q99L32 mus musculu
10	91	47.9	481	11 Q88947	Q88947 mus musculu
11	85	44.7	100	4 Q15253	Q15253 homo sapien
12	81	42.6	49	6 Q95ME8	Q95ME8 bos taurus
13	80	42.1	456	4 Q14316	Q14316 homo sapien
14	80	42.1	461	6 Q95ND7	Q95ND7 pan troglod
15	80	42.1	461	6 Q95ND6	Q95ND6 pan troglod
16	76	40.0	179	4 Q87RAS3	Q87RAS3 homo sapien

17	76	40.0	198	11 Q8R182	Q8R182 mus musculu
18	74	38.9	138	6 Q28994	Q28994 sus scrofa
19	70	36.8	433	13 Q90YK1	Q90YK1 brachydanto
20	67	35.3	648	6 Q29094	Q29094 sus scrofa
21	65	34.2	98	13 P82807	P82807 notechis sc
22	64	33.7	399	11 Q9COW3	Q9COW3 mus musculu
23	63	33.2	608	13 Q9PTW7	Q9PTW7 struthio ca
24	62	32.6	650	4 Q9NSD0	Q9NSD0 homo sapien
25	62	32.6	650	4 Q16519	Q16519 homo sapien
26	60	31.6	607	13 Q91001	Q91001 gallus gall
27	58.5	30.8	431	10 Q94E15	Q94E15 arabisdops
28	58.5	30.8	492	10 Q9SMU7	Q9SMU7 cicier arter
29	58.5	30.8	543	10 Q9MB23	Q9MB23 arabisdops
30	58.5	30.8	576	10 Q9C9U4	Q9C9U4 arabisdops
31	58.5	30.8	589	10 Q9LMS2	Q9LMS2 arabisdops
32	57.5	30.3	196	10 Q04284	Q04284 selaginella
33	57.5	30.3	542	5 Q8T613	Q8T613 halocynthia
34	56.5	29.7	459	10 Q9SE22	Q9SE22 oryza sativ
35	55.5	29.2	506	10 Q9SPF0	Q9SPF0 oryza sativ
36	55.5	29.2	506	10 Q9SE23	Q9SE23 oryza sativ
37	55.5	29.2	567	10 Q8M4J2	Q8M4J2 arabisdops
38	55	28.9	25	11 Q9QVH6	Q9QVH6 rattus sp.
39	54.5	28.7	510	10 Q9MB22	Q9MB22 arabisdops
40	54.5	28.7	619	10 Q9LV37	Q9LV37 arabisdops
41	53	27.9	673	11 Q61592	Q61592 mus musculu
42	53	27.9	674	11 Q99K57	Q99K57 mus musculu
43	52.5	27.6	588	10 Q9LM33	Q9LM33 arabisdops
44	52.5	27.6	603	10 Q9LPG7	Q9LPG7 arabisdops
45	52.5	27.6	606	10 Q9SUG9	Q9SUG9 arabisdops

ALIGNMENTS

RESULT 1
Q96P08 PRELIMINARY: PRT: 701 AA.
AC Q96P08: 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAK58686.1; -.
DR InterPro: IPR000152; Asx hydrolase.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001254; Ser protease_Try.
DR InterPro: IPR000294; Vltk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00447; ig; 2.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SMO0181; EGF_2.
DR PROSITE: PS00010; Asx hydroxyl; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC92F CRC64;

Query Match 83.7%; Score 159; DB 4; Length 701;
 Best Local Similarity 72.7%; Pred. No. 8e-21;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXXQCSFXXAEXIFKDAKTKLFWISY 44
 DB 61 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 2
 O61109 PRELIMINARY; PRT; 446 AA.

ID O61109; AC O61109; DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Coagulation factor VII.
 GN F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.,
 RT Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY
 CC EMBL: U44795; AAC52570.1; -.
 DR HSSP; P08709; 1FAK.
 DR MGD; MGI:109325; F7.
 DR InterPro: IPR002086; Aldehyde dehydr.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00225; CRYSTALLIN BETAGANMA; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 60.0%; Score 114; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXXQCSFXXAEXIFKDAKTKLFWISY 44
 DB 42 ANSLEELWPGSLRECKNECCSFEEAREIFKSPERTKQFWIVY 85

RESULT 3

ID Q91WN8 PRELIMINARY; PRT; 460 AA.

AC Q91WN8; DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC013896; AH13896.1; -.
 DR MGD; MGI:97771; Proc.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117P2E686FCC274 CRC64;

Query Match 53.7%; Score 102; DB 11; Length 460;
 Best Local Similarity 45.5%; Pred. No. 2.2e-10;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXXQCSFXXAEXIFKDAKTKLFWISY 44
 DB 42 ANSLEELWPGSLRECKNECCSFEEAREIFQWVEDTLAWIKY 85

RESULT 4

ID Q99PC6 PRELIMINARY; PRT; 460 AA.

AC Q99PC6; DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;


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DR InterPro: IPR000294; VitC_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; EGF_2.
DR SMART: SM00020; GLA_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR KMW: Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42 POTENTIAL
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 48.4%; Score 92; DB 6; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.6e-08;
Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXREGSLKRXCKXXQCSFXAXEIXFKDAXRTKLFWISY 44
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 43 ANSLFEIRAGSLERECMEICDEEAKETFGVNDTLTAVSKY 86

RESULT 7
O9GMD9 PRELIMINARY; PRT; 469 AA.
AC O9GMD9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; Pubmed=1132153;
RT "Identification and structural analysis of four serine proteases in a
   monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
   TRYPSIN FAMILY.
EMBL: AF275654; AAC00453.1; -.
DR HSSP; P00742; 1XKB.
DR MEROPS; S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitC_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA_1.

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DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR KMW: Hydroxylase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C23D0D758F6A CRC64;

Query Match 47.9%; Score 91; DB 6; Length 469;
Best Local Similarity 36.4%; Pred. No. 2.6e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXREGSLKRXCKXXQCSFXAXEIXFKDAXRTKLFWISY 44
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 41 ANSLFEELKKNLFRFCNERTCSYEAREVFEEDTDTNTERFWNY 84

RESULT 8
O54740 PRELIMINARY; PRT; 481 AA.
AC O54740;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR FAL0.
OS Mus musculus (Mouse).
OG Elasmobranchii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; Pubmed=9783672;
RA Heidemann H.H.; Kontemann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
   TRYPSIN FAMILY.
EMBL: AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitC_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.

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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DSEFP9D7AE CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 2.7e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXAEXIFKDAKRTKLFWISY 44
Db 41 ANSFEEFKGNLRRCMEICSYEEVREIFEDDEKTKYWKY 84

RESULT 9
Q99L32 PRELIMINARY; PRT; 481 AA.
AC Q99L32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 2.7e-08;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRGSLRXCKXQCSFXAEXIFKDAKRTKLFWISY 44
Db 41 ANSFEEFKGNLRRCMEICSYEEVREIFEDDEKTKYWKY 84

RESULT 10
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update).
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RT Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL; AF087644; AAC6345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09DE5EF9D271E CRC64;

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
133.780 Million cell updates/sec

Title: 10GLU28GLU

Perfect score: 190

Sequence: 1 ANAFLXLRREGSLXRCCKX.....XXAEXIFKDXRTLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.8	44	3	US-08-955-636-26
2	162	85.3	44	3	US-08-955-636-27
3	159	83.7	44	3	US-08-955-636-3
4	159	83.7	406	1	US-08-293-778-24
5	159	83.7	406	1	US-08-295-411-5
6	159	83.7	406	2	US-08-955-471-5
7	159	83.7	444	5	PCT-US92-10242-5
8	159	83.7	444	1	US-08-475-845-2
9	159	83.7	444	2	US-08-327-690-2
10	159	83.7	444	2	US-08-660-289-2
11	159	83.7	444	2	US-08-537-807-2
12	159	83.7	444	2	US-08-871-003-2
13	159	83.7	444	2	US-08-464-233-2
14	159	83.7	444	4	US-09-189-607-2
15	159	83.7	444	4	US-09-378-907-2
16	159	83.7	444	5	PCT-US94-05779-2
17	159	83.7	466	1	US-07-882-202A-4
18	159	83.7	466	1	US-08-021-615A-4
19	159	83.7	466	1	US-08-321-777-4
20	159	83.7	466	4	US-09-009-217-14
21	159	83.7	466	4	US-09-009-655-14
22	159	83.7	466	5	PCT-US93-04493-4
23	158	83.2	44	3	US-08-955-636-30
24	156	82.1	44	3	US-08-955-636-28
25	153	80.5	44	3	US-08-955-636-29
26	144	75.8	41	1	US-08-229-280-4
27	123	64.7	44	3	US-08-955-636-4

28	108	56.8	139	1	US-08-330-978-2	Sequence 2, Appli
29	108	56.8	139	1	US-08-474-042-2	Sequence 2, Appli
30	108	56.8	139	1	US-08-484-558-2	Sequence 2, Appli
31	108	56.8	139	1	US-08-774-592-2	Sequence 2, Appli
32	108	56.8	437	1	US-08-487-037-2	Sequence 2, Appli
33	108	56.8	437	1	US-08-487-037-3	Sequence 3, Appli
34	108	56.8	488	1	US-08-487-037-1	Sequence 3, Appli
35	101	53.2	44	3	US-08-955-636-35	Sequence 35, Appli
36	99	52.1	44	3	US-08-955-636-18	Sequence 18, Appli
37	99	52.1	448	1	US-08-295-411-3	Sequence 3, Appli
38	99	52.1	448	2	US-08-955-471-3	Sequence 3, Appli
39	99	52.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
40	99	52.1	448	5	PCT-US92-10242-3	Sequence 53, Appli
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42	99	52.1	487	2	US-08-469-486-53	Sequence 2, Appli
43	99	52.1	492	1	US-08-469-486-2	Sequence 2, Appli
44	99	52.1	492	2	US-08-469-486-2	Sequence 2, Appli
45	98	51.6	44	3	US-08-955-636-24	Sequence 24, Appli

ALIGNMENTS

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RESULT 1
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      86.8%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.2e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXLRREGSLXRCCKXCSFYXAXEIPKDXRTLFWISY 44
Db 1 ANAFLXLRREGSLXRCCKXCSFYXAXEIPKDXRTLFWISY 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match
Best Local Similarity 95.5%; Score 162; DB 3; Length 44;
Pred. No. 3.9e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44

RESULT 3
US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match
Best Local Similarity 95.5%; Score 159; DB 3; Length 44;
Pred. No. 1.2e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44

RESULT 4
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wibergh, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560ch America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agrie, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match
Best Local Similarity 72.7%; Score 159; DB 1; Length 406;
Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLLYLRGSLYRXCKYQCSFYVARYIFPDVARTKLFWISY 44

RESULT 5
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Masters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas


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;
;   REGISTRATION NUMBER: 34,163
;   REFERENCE/DOCKET NUMBER: TSR1263.0C1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-554-2937
;   TELEFAX: 619-554-6312
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
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;   FEATURe:
;   NAME/KEY: Region
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-295-471-5

Query Match      83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLXRCXKXOCSPXAXEIPFDARTKLFWISY 44
Db 1 ANAFLELRPGSLRCKEBCQSFEBAREIFPDARTKLFWISY 44

RESULT 6
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffen, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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;
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
;
;   FEATURe:
;   NAME/KEY: Region
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-955-471-5

Query Match      83.7%; Score 159; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLXRCXKXOCSPXAXEIPFDARTKLFWISY 44
Db 1 ANAFLELRPGSLRCKEBCQSFEBAREIFPDARTKLFWISY 44

RESULT 7
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffen, John H.
; APPLICANT: Meesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR0472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
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OTHER INFORMATION: /note="Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note="Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match      83.7%; Score 159; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLXXLRGSLRXCKXQCSFXAEXIFKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-08-475-845-2
; Sequence 2, Application US/08475845
; Patent No. 5788965
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,845
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-845-2

Query Match      83.7%; Score 159; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
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Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLXXLRGSLRXCKXQCSFXAEXIFKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 39 ANAFLLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 9
US-08-327-690-2
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-327-690-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLXXLRGSLRXCKXQCSFXAEXIFKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 39 ANAFLLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
```

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; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,269
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475, 845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXCKXQCSFXXAEXIFKDXARTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEARLTFKDAERTKLFWISY 82

RESULT 11
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXCKXQCSFXXAEXIFKDXARTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEARLTFKDAERTKLFWISY 82

RESULT 12
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAERTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 83.7%; Score 159; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAERTKLFWISY 44

DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-189-607-2

Query Match 83.7%; Score 159; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAERTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-09-378-907-2
Sequence 2, Application US/09378907
Patent No. 6183743

```
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,907
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/871,003
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-378-907-2

Query Match      83.7%; Score 159; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 ANAFLLXLRSGSLRXCKXKCSFXXAEKIFDAXRTKLFWISY 44
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Db      39 ANAFLEELRPGSLRRCRCKQCSFEAEKIFDAXRTKLFWISY 82
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Search completed: March 19, 2003, 15:16:12
Job time : 10.75 secs

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

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Perfect score: 190
Sequence: 1 ANAFLXXLRGSLKRXCKX.....XXAEXIFDXRXTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues
Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	159	83.7	406	US-10-109-498-1	Sequence 1, Appli
2	98	51.6	419	US-10-182-263-6	Sequence 6, Appli
3	96	50.5	419	US-10-182-263-3	Sequence 3, Appli
4	96	50.5	419	US-10-182-263-4	Sequence 4, Appli
5	96	50.5	419	US-10-182-263-5	Sequence 5, Appli
6	85	44.7	419	US-10-182-263-1	Sequence 1, Appli
7	85	44.7	419	US-09-978-917A-4	Sequence 4, Appli
8	85	44.7	461	US-10-182-263-2	Sequence 2, Appli
9	85	44.7	461	US-09-978-917A-2	Sequence 2, Appli
10	80	42.1	415	US-09-118-748-2	Sequence 2, Appli
11	80	42.1	461	US-10-132-829-5	Sequence 5, Appli
12	80	42.1	461	US-09-884-901-3	Sequence 3, Appli
13	69.5	36.6	96	US-09-759-130B-113	Sequence 313, App
14	69.5	36.6	209	US-09-759-130B-112	Sequence 312, App
15	69.5	36.6	226	US-09-759-130B-110	Sequence 310, App
16	54.5	28.7	908	US-09-759-130B-356	Sequence 356, App
17	54.5	28.7	208	US-09-759-130B-355	Sequence 355, App
18	54.5	28.7	225	US-09-759-130B-353	Sequence 353, App
19	45	23.7	273	US-09-764-868-968	Sequence 968, App

20	44	23.2	447	10	US-09-815-242-13490	Sequence 13490, A
21	44	23.2	447	10	US-09-815-242-13612	Sequence 13612, A
22	44	23.2	447	10	US-09-735-564-2	Sequence 2, Appli
23	43	22.6	88	10	US-09-811-284-194	Sequence 194, App
24	43	22.6	1266	9	US-09-931-969A-2	Sequence 2, Appli
25	43	22.6	1266	9	US-10-079-699-2	Sequence 2, Appli
26	43	22.6	1266	10	US-09-757-781-63	Sequence 63, Appli
27	43	22.6	1356	10	US-09-757-781-2	Sequence 2, Appli
28	42	22.1	608	10	US-09-908-664-5	Sequence 5, Appli
29	42	22.1	729	9	US-10-145-396-11	Sequence 11, Appli
30	42	22.1	1258	10	US-09-922-943-1	Sequence 1, Appli
31	42	22.1	1274	10	US-09-746-491-12	Sequence 8, Appli
32	41.5	21.8	440	9	US-09-910-186A-8	Sequence 1, Appli
33	40.5	21.3	744	10	US-09-969-528-5	Sequence 5, Appli
34	40	21.1	744	10	US-09-862-179A-1	Sequence 1, Appli
35	40	21.1	924	12	US-10-028-056-5	Sequence 5, Appli
36	40	21.1	1337	10	US-09-757-781-62	Sequence 62, Appli
37	39	20.5	347	10	US-09-780-053-4	Sequence 4, Appli
38	39	20.5	730	9	US-10-145-396-12	Sequence 12, Appli
39	39	20.5	730	10	US-09-780-053-2	Sequence 2, Appli
40	39	20.5	873	9	US-10-200-154-2	Sequence 2, Appli
41	39	20.5	873	10	US-09-954-043-2	Sequence 2, Appli
42	38.5	20.3	49	10	US-09-764-864-1054	Sequence 1054, App
43	38.5	20.3	348	10	US-09-982-510-18	Sequence 18, Appli
44	38.5	20.3	1298	10	US-09-982-510-33	Sequence 33, Appli
45	38.5	20.3	1363	9	US-09-375-248-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      83.7%; Score 159; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 1.2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ANAFLXXLRGSLKRXCKXQCSFXAEXIFDXRXTLFWISY 44
Db 1 ANAFLXXLRGSLKRXCKXQCSFXAEXIFDXRXTLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022154A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
```

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          51.6%; Score 98; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.2e-09;
Matches 20; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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Db 1 ANSFLELRHGSLEKCEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

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Db 1 ANSFLELRHGSLEKCEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.7e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41
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RESULT 7
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u810 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.7e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41
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Db 1 ANSFLELRHSSLRERCIEICDFEAKETFOVVDTLAFW 41

RESULT 8
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match          44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 3e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

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RESULT 9

; ORGANISM: Homo sapiens
US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u810 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match          44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 3e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41
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Db 43 ANSFLELRHSSLRERCIEICDFEAKETFOVVDTLAFW 83

RESULT 10
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jindl
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match          42.1%; Score 80; DB 10; Length 415;
Best Local Similarity 40.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 10 EGSLLRXCKXQCSFXXAEXIFKDXARTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 11
US-10-133-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-Pal170
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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          42.1%; Score 80; DB 9; Length 461;
Best Local Similarity 40.0%; Pred. No. 2.4e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy      10 EGSIXRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      57 QGNLERECMEKCSFEAREVFEVTERTEFTFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: WO/99-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match          42.1%; Score 80; DB 10; Length 461;
Best Local Similarity 40.0%; Pred. No. 2.4e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy      10 EGSIXRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      57 QGNLERECMEKCSFEAREVFEVTERTEFTFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          36.6%; Score 69.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 3.5e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

Qy      2 NAF-LXXLRGSLXRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      36 NRPDLLEFTPGNLERECNEELCNVEAREIFVDEDXTIAFWQRY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-130B-312

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Best Local Similarity 36.4%; Pred. No. 8.1e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2  NAF-LXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFWISY 44
Db      36  NRFDLELFTPGNLERECNELCNVEEARLIFVDEDKTIATFMOEY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US0030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350N1M
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
; US-09-759-130B-310

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Best Local Similarity 36.4%; Pred. No. 8.8e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2  NAF-LXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFWISY 44
Db      53  NRFDLELFTPGNLERECNELCNVEEARLIFVDEDKTIATFMOEY 96

Search completed: March 20, 2003, 13:30:09
Job time : 9.375 secs
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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.865 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFLXLRKSLRXKCKX.....XXAFYFKDAXRKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	165	86.4	44	20	AAV18312	Modified GLA domain
2	162	84.8	44	20	AAV18310	Modified GLA domain
3	159	83.2	44	20	AAV18311	Modified GLA domain
4	156	81.7	44	20	AAV18305	Human factor VII G
5	156	81.7	44	22	AAV18395	Human factor VII G
6	156	81.7	401	22	AAV18470	Mutant blood coagu
7	156	81.7	401	22	AAV18471	Mutant blood coagu
8	156	81.7	406	14	AAV185764	Factor VII (VII).
9	156	81.7	406	18	AAV14509	Modified blood coa
10	156	81.7	406	18	AAV14510	Modified blood coa

11	156	81.7	406	22	AAV77745	Human factor VIIa
12	156	81.7	406	22	AAV52171	Human FVII SEQ ID
13	156	81.7	406	22	AAV52172	Mammalian expresse
14	156	81.7	406	22	AAV52181	Human FVII mutant
15	156	81.7	406	22	AAV52182	Human FVII mutant
16	156	81.7	406	22	AAV52183	Human FVII mutant
17	156	81.7	406	22	AAV52184	Human FVII mutant
18	156	81.7	406	22	AAV52185	Human FVII mutant
19	156	81.7	406	22	AAV52186	Human FVII mutant
20	156	81.7	406	22	AAV52187	Human FVII mutant
21	156	81.7	406	22	AAV52188	Human FVII mutant
22	156	81.7	406	22	AAV52189	Human FVII mutant
23	156	81.7	406	22	AAV52190	Human FVII mutant
24	156	81.7	406	22	AAV52191	Human FVII mutant
25	156	81.7	406	22	AAV52192	Human FVII mutant
26	156	81.7	406	22	AAV52193	Human FVII mutant
27	156	81.7	406	22	AAV52194	Human FVII mutant
28	156	81.7	406	22	AAV52195	Human FVII mutant
29	156	81.7	406	22	AAV52196	Human FVII mutant
30	156	81.7	406	22	AAV52197	Human FVII mutant
31	156	81.7	406	22	AAV52198	Human FVII mutant
32	156	81.7	406	22	AAV52199	Human FVII mutant
33	156	81.7	406	22	AAV52200	Human FVII mutant
34	156	81.7	406	22	AAV52201	Human FVII mutant
35	156	81.7	406	22	AAV52202	Human FVII mutant
36	156	81.7	406	22	AAV52203	Human FVII mutant
37	156	81.7	406	22	AAV52204	Human FVII mutant
38	156	81.7	406	22	AAV52205	Human FVII mutant
39	156	81.7	406	22	AAV52206	Human FVII mutant
40	156	81.7	406	22	AAV52207	Human FVII mutant
41	156	81.7	406	22	AAV52208	Human FVII mutant
42	156	81.7	406	22	AAV52209	Human FVII mutant
43	156	81.7	406	22	AAV52210	Human FVII mutant
44	156	81.7	406	22	AAV52211	Human FVII mutant
45	156	81.7	406	22	AAV52212	Human FVII mutant

ALIGNMENTS

RESULT 1	AAV18312	standard; peptide; 44 AA.
ID	AAV18312	
AC	AAV18312;	
DT	17-AUG-1999	(first entry)
XX		
DE	Modified GLA domain of vitamin K-dependent protein.	
XX		
KW	GLA domain; muten; vitamin K-dependent protein; clotting disorder;	
XX		
OS	therapy.	
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	FT	note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX		
PN	MO9920767-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	20-OCT-1998; 98WO-US22152.	
XX		
PR	23-OCT-1997; 97US-0955636.	
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
PI	Nelsetuen GL;	
XX		

DR WPI; 1999-288309/24.
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 SQ Sequence 44 AA;
 Query Match 86.4%; Score 165; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 3e-20; Mismatches 0; Gaps 0;
 Matches 43; Conservative 0; Indels 0; Deletions 0;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 DB
 RESULT 2
 AAY18310
 ID AAY18310 standard; peptide; 44 AA.
 XX
 XX AAY18310;
 DT 17-AUG-1999 (first entry)
 XX
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 acid"
 XX
 XX
 PN WO9920767-A1.
 XX
 XX
 XX 29-APR-1999.
 PD
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 XX 20-OCT-1998; 98WO-US22152.
 PF
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 PR 23-OCT-1997; 97US-0955636.
 PA (MINU) UNIV MINNESOTA.
 XX
 XX
 PI Nelstuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC

CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 SQ Sequence 44 AA;
 Query Match 84.8%; Score 162; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 9.6e-20;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 DB
 RESULT 3
 AAY18311
 ID AAY18311 standard; peptide; 44 AA.
 XX
 XX AAY18311;
 AC
 XX
 DT 17-AUG-1999 (first entry)
 XX
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 acid"
 XX
 XX
 PN WO9920767-A1.
 XX
 XX
 XX 29-APR-1999.
 PD
 XX
 XX 20-OCT-1998; 98WO-US22152.
 PF
 XX
 PR 23-OCT-1997; 97US-0955636.
 PA (MINU) UNIV MINNESOTA.
 XX
 XX
 PI Nelstuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 SQ Sequence 44 AA;
 Query Match 83.2%; Score 159; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 3.1e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 1 ANAFLXXLRGSLXRCCKXXQCSFXXAFXIFKDXARTLFWISY 44
 DB

```

RESULT 4
AAV18305
ID AAV18305 standard; peptide; 44 AA.
XX
XX
AC AAV18305;
XX
XX
DT 17-AUG-1999 (first entry)
XX
XX
DE Human factor VII GLA domain.
XX
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder;
therapy.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa=gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
XX
XX
PM WO920767-A1.
XX
XX
PD 29-APR-1999.
XX
XX
PF 20-OCT-1998; 98WO-US22152.
XX
XX
PR 23-OCT-1997; 97US-0955636.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PI Nelstuen GL;
XX
XX
DR WPI, 1999-288309/24.
XX
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX
PS Disclosure; Page 15; 86pp; English.
XX
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX
SQ Sequence 44 AA;
XX
XX
Query Match 81.7%; Score 156; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 9.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFDAXRTKLFWISY 44
Db 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFDAXRTKLFWISY 44
XX
XX
RESULT 5
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX
AC AAB36395;
XX
XX
DT 27-FEB-2001 (first entry)
XX
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
factor X; prothrombin; enhanced membrane binding affinity;
XX

```

```

KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
XX
OS Homo sapiens.
XX
XX
PM WO200066753-A2.
XX
XX
PD 09-NOV-2000.
XX
XX
PF 28-APR-2000; 2000WO-US11416.
XX
XX
PR 29-APR-1999; 99US-0302239.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PI Nelstuen GL;
XX
XX
DR WPI, 2001-007226/01.
XX
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity
XX
XX
PS Disclosure; Page 12; 81pp; English.
XX
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX
SQ Sequence 44 AA;
XX
XX
Query Match 81.7%; Score 156; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 9.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFDAXRTKLFWISY 44
Db 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFDAXRTKLFWISY 44
XX
XX
RESULT 6
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX
AC AAB84870;
XX
XX
DT 31-JUL-2001 (first entry)
XX
XX
DE Mutant blood coagulant factor VII (FVII-31).
XX
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
mutant; mutein.
XX
XX
OS Homo sapiens.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX

```

PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-0237610.
 XX
 PR 24-AUG-1999; 99JP-0237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 the treatment of hemophilia -
 XX
 PS Claim 14, Page 20-21; 29pp; Japanese.
 XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX
 SQ Sequence 401 AA;
 XX
 Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 9.2e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 QY 1 ANAFLLXLRGSLKRXCKXQCSFXAXFXIPKDXRTKLFWISY 44
 |||||
 1 ANAFLELRPGSLERCKEQCSFEAREIKDARTKLFWISY 44
 Db
 XX
 RESULT 7
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.
 XX
 AC AAB84871;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutsin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 FT Asp-Arg-Lys-Thr-Leu"
 FT MISC-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 FT
 XX
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-0237610.
 XX
 PR 24-AUG-1999; 99JP-0237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 the treatment of hemophilia -

XX
 PS Claim 15, Page 23-24; 29pp; Japanese.
 XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX
 SQ Sequence 401 AA;
 XX
 Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 9.2e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 QY 1 ANAFLLXLRGSLKRXCKXQCSFXAXFXIPKDXRTKLFWISY 44
 |||||
 1 ANAFLELRPGSLERCKEQCSFEAREIKDARTKLFWISY 44
 Db
 XX
 RESULT 8
 AAR35764
 ID AAR35764 standard; protein; 406 AA.
 XX
 AC AAR35764;
 XX
 DT 24-SEP-1993 (first entry)
 XX
 DE Factor VII (VII).
 XX
 KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
 KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
 KW exosite; catalytic activity.
 XX
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 1..152
 FT /note= "Factor VII light chain"
 FT Region 153..406
 FT /note= "Factor VII heavy chain"
 FT Peptide 374..388
 FT /note= "exosite 1"
 FT Peptide 290..310
 FT /note= "exosite 2"
 FT Peptide 290..310
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 FT Peptide 374..388
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 FT Peptide 289..304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 290..304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 245..266
 FT /note= "claim 9, page 138-139 describes an antibody
 FT that reacts with Factor VII; fragments
 FT 289-304, 290-304, 290-310, 374-388 and
 FT 400-414 but not with fragment 245-266"
 FT
 XX
 PN WO9309804-A.
 XX
 PD 27-MAY-1993.
 XX
 PF 18-NOV-1992; 92WO-US10242.
 XX
 PR 18-NOV-1991; 91US-0793989.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 FI Grifflin JH, Meesters RM;
 XX
 DR WPI; 1993-182244/22.
 XX
 PT Serine protease derived-polypeptide(s) and anti-peptide

PT antibodies - for inhibiting coagulation and assaying for the
 PT presence of serine protease in fluid samples
 XX
 PS Disclosure; Page 133-135; 149pp; English.
 XX
 CC The PC polypeptides indicated in the Features Table inhibit
 CC coagulation (they prevent binding of serine protease to natural
 CC substrates), esp. when admin. to give an intravascular blood
 CC concn. of 0.1-100 (pref. 0.5-10) microM.
 CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
 CC in the specification but have not yet been added to the SEQUENCE
 CC LISTING.
 CC
 XX
 SQ Sequence 406 AA;
 XX
 Query Match 81.7%; Score 156; DB 14; Length 406;
 Best Local Similarity 72.7%; Pred. No. 9.3e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ANAFLLXRLREGSLRXCKXKQCSFXAXFIFKDXARTKLPWISY 44
 Db 1 ANAFLELRGSLERECKEQCSFEERARLFXDAERTKLPWISY 44
 RESULT 9
 AAW14509
 ID AAW14509 standard; protein; 406 AA.
 AC AAW14509;
 XX
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (R290S).
 XX
 KM Blood coagulation; factor 7; mutein; mutation; modification;
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Disulfide-bond
 FT 17..22
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Cleavage-site
 FT 32..33
 FT /note= "proteolytic site"
 FT Modified-site
 FT /label= OTHER

FT /note= "gamma-carboxylutamic acid"
 FT 38..39
 FT /note= "proteolytic site"
 FT Cleavage-site
 FT 42..43
 FT /note= "proteolytic site"
 FT Cleavage-site
 FT 44..45
 FT /note= "proteolytic site"
 FT Disulfide-bond
 FT 50..61
 FT Disulfide-bond
 FT 55..70
 FT Modified-site
 FT 63
 FT /label= OTHER
 FT /note= "beta-hydroxy-aspartic acid"
 FT Disulfide-bond
 FT 72..81
 FT Disulfide-bond
 FT 91..102
 FT Disulfide-bond
 FT 98..112
 FT Disulfide-bond
 FT 114..127
 FT Disulfide-bond
 FT 135..162
 FT Cleavage-site
 FT 143..144
 FT /note= "proteolytic site"
 FT Modified-site
 FT 145
 FT /note= "glycosylation site"
 FT Disulfide-bond
 FT /note= "glycosylation site"
 FT Disulfide-bond
 FT 159..164
 FT Disulfide-bond
 FT 178..194
 FT Active-site
 FT 193
 FT Active-site
 FT 242
 FT Active-site
 FT 344
 FT Cleavage-site
 FT 290..291
 FT /note= "proteolytic site in unmodified factor VII"
 FT Misc-difference
 FT 290
 FT /note= "native Arg290 has been substituted by Ser to
 FT provide a proteolytically more stable peptide
 FT bond"
 FT Disulfide-bond
 FT 310..329
 FT Cleavage-site
 FT 315..316
 FT /note= "proteolytic site"
 FT Modified-site
 FT 322
 FT /note= "glycosylation site"
 FT Disulfide-bond
 FT 340..368
 FT Cleavage-site
 FT 341..342
 FT /note= "proteolytic site"
 FT Cleavage-site
 FT 392..393
 FT /note= "proteolytic site"
 FT Cleavage-site
 FT 396..397
 FT /note= "proteolytic site"
 FT Cleavage-site
 FT 402..403
 FT /note= "proteolytic site"
 FT
 XX US5580560-A.
 XX
 XX
 XX 03-DEC-1996.
 XX
 XX
 XX 13-NOV-1989; 89US-0434149.
 XX
 XX 09-AUG-1993; 93US-0104509.
 XX 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0898248.
 PR 22-AUG-1994; 94US-0293778.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
 XX WPI; 1997-033523/03.
 XX
 XX Mutated human factor VII or VIIA proteins - with amino acid
 XX substitutions to improve proteolytic stability
 XX
 PS Example 3; Page -, 28pp; English.
 XX
 CC Modified human factor VII or VIIA proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable

CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.

XX Sequence 406 AA;

Query Match 81.7%; Score 156; DB 18; Length 406;
 Best Local Similarity 72.7%; Pred. No. 9.3e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AANFLXXLRGSLKRXKXQCSFXAFLFKDAXRTKFLWISY 44
 1 AANFLBELRPGSLERCKECSFEERAREIFKDAERTKFLWISY 44
 Db

RESULT 10
 AAM14510
 ID AAM14510 standard; protein; 406 AA.

XX AAM14510;

DT 14-MAY-1997 (first entry)

XX Modified blood coagulation Factor VII (R315S).

KM Blood coagulation; factor 7; mutein; mutation; modification;
 KW thrombocytopenia; von Willebrand's disease; plasma substitute.

XX Homo sapiens.
 OS Synthetic.

XX Location/Qualifiers

FT Modified-site

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"

FT /note= "proteolytic site"
 FT 50..61
 FT Disulfide-bond
 FT 55..70
 FT Modified-site
 FT /label= OTHER

FT /note= "beta-hydroxy-aspartic acid"

FT Disulfide-bond

FT 72..81

FT Disulfide-bond

FT 91..102

FT Disulfide-bond

FT 98..112

FT Disulfide-bond

FT 114..127

FT Disulfide-bond

FT 135..162

FT Disulfide-bond

FT 143..144

FT Cleavage-site

FT /note= "proteolytic site"

FT Modified-site

FT 145

FT /note= "glycosylation site"

FT Disulfide-bond

FT 159..164

FT Disulfide-bond

FT 178..194

FT Active-site

FT 193

FT Active-site

FT 242

FT Active-site

FT 344

FT Cleavage-site

FT 290..291

FT /note= "proteolytic site"

FT Disulfide-bond

FT 310..329

FT Cleavage-site

FT 315..316

FT /note= "proteolytic site in unmodified factor VII"

FT Misc-difference

FT 315

FT /note= "native Arg315 has been substituted by Ser to
 provide a proteolytically more stable peptide
 bond"

FT Modified-site

FT 322

FT /note= "glycosylation site"

FT Disulfide-bond

FT 340..368

FT Cleavage-site

FT 341..342

FT /note= "proteolytic site"

FT Cleavage-site

FT 392..393

FT /note= "proteolytic site"

FT Cleavage-site

FT 396..397

FT /note= "proteolytic site"

FT Cleavage-site

FT 402..403

FT /note= "proteolytic site"

FT /note= "proteolytic site"

XX US580560-A.

XX PN

XX 03-DEC-1996.

XX PD

XX 13-NOV-1989;

XX PF 89US-0434149.

XX XX

PR 09-AUG-1993;

PR 93US-0104509.

PR 13-NOV-1989;

PR 89US-0434149.

PR 12-JUN-1992;

PR 92US-0898248.

PR 22-AUG-1994;

PR 94US-0293778.

XX XX

PA (NOVO) NOVO-NORDISK AS.

XX XX

PI Bjorn SE, Nicolsaesen EM, Wiberg FC, Woodbury R;

XX WPI; 1997-033523/03.

XX Mutated human factor VII or VIIa proteins - with amino acid
 substitutions to improve proteolytic stability

XX Example 4; Page -; 28pp; English.

XX Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.

```
XX SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 9.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFKIFKDAKRTKLFMISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLEELRPGSLERCKECCSFEPARFIKDAERTKLFMISY 44

RESULT 11
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX AAU77745;
AC AAU77745;
DT 05-JUN-2002 (first entry)
XX
DE Human factor VIIa active site mutant.
XX
KW Factor VIIa; human; shock heat treatment; protein stability;
KW protein manufacture; protein conformation; mutant; mutlein.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FH Active-site 193
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344
FT /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala. Wild type Ser"
XX
PN WO200177141-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-DK00234.
XX
PR 06-APR-2000; 2000DK-0000573.
PR 17-APR-2000; 2000US-197650P.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Mathiesen F;
XX
DR WPI; 2001-657162/75.
XX
PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment -
XX
PS Disclosure; Page -; 22pp; English.
XX
CC The invention describes a method of stabilising a polypeptide involving
CC shock heat treatment of the polypeptide. The method is useful in a
CC pharmaceutical composition, in the industrial or large scale method of
CC manufacturing a polypeptide, also as a unit operation during preparation,
CC purification, recovery and/or formulation of polypeptides. The shock heat
CC treatment improves the protein stability without substantial loss of
CC biological activity. The method can be applied to change polypeptide
CC conformation in a very fast and non-invasive manner. The polypeptide
CC formed is stable. The method is also useful for decreasing the
CC association of the polypeptide. This sequence represents a modified
CC human factor VIIa protein, mutated at the catalytic site, described
CC in the invention.
CC Note: This sequence does not appear in the specification but has
CC been obtained using information given in the invention.
```

```
XX SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 9.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFKIFKDAKRTKLFMISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLEELRPGSLERCKECCSFEPARFIKDAERTKLFMISY 44

RESULT 12
AAM52171
ID AAM52171 standard; Protein; 406 AA.
XX AAM52171;
AC AAM52171;
DT 07-FEB-2002 (first entry)
XX
DE Human FVII SEQ ID NO 1.
XX
KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiac; hepatocytic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Misc-difference 6
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 7
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 14
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 16
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 19
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 20
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 25
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 26
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 29
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 35
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Modified-site 52
FT /note= "O-glycosylated"
FT Modified-site 60
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "N-glycosylated"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
PN WO200158935-A2.
```

```

XX 16-AUG-2001.
PD
XX
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX MPI: 2001-581807/65.
XX
XX N-PSDB; AA199982.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Claim 1; Page 81-83; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 81.7%; Score 156; DB 22; Length 406;
XX Best Local Similarity 95.5%; Pred. No. 9.3e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ANAFLLXLRBGSILRXCKXQCSFXAXFXFKDAXRTKLFWISY 44
QY
XX 1 ANAFLLXLRBGSILRXCKXQCSFXAXFXFKDAXRTKLFWISY 44
Db
XX
XX RESULT 13
XX AAM52172 standard; Protein; 406 AA.
XX
XX AAM52172;
XX
XX 07-FEB-2002 (first entry)
XX
XX Mammalian expressed human FVII SEQ ID NO 3.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 52 /note= "O-glycosylated"
XX Modified-site 60 /note= "O-glycosylated"
XX Modified-site 145 /note= "N-glycosylated"
XX Cleavage-site 152..153
FT

```

```

FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322 /note= "N-glycosylated"
XX
XX MO200158935-A2.
XX
XX 16-AUG-2001.
PD
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX MPI: 2001-581807/65.
XX
XX N-PSDB; AA199983.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Disclosure; Page 85-86; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 81.7%; Score 156; DB 22; Length 406;
XX Best Local Similarity 72.7%; Pred. No. 9.3e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1 ANAFLLXLRBGSILRXCKXQCSFXAXFXFKDAXRTKLFWISY 44
QY
XX 1 ANAFLEELRPGSLERBECKECSFEERARLIFKDAERTKLFWISY 44
Db
XX
XX RESULT 14
XX AAM52181 standard; Protein; 406 AA.
XX
XX AAM52181;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII mutant T106N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX
XX Homo sapiens.
XX
XX Synthetic.
OS

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 / Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28PNE
Perfect score: 191
Sequence: 1 ANAFLLXLRREGSLXRXCKX.....XXAFXFKDAXRKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	1 KFHU7	coagulation factor
2	122	63.9	443	2 I46932	coagulation factor
3	114	59.7	407	1 KFB07	coagulation factor
4	97	50.8	461	1 JX0210	protein C (activat
5	96	50.3	461	1 S18994	protein C (activat
6	96	50.3	488	1 EXHU	coagulation factor
7	96	50.3	492	1 EXBO	coagulation factor
8	94	49.2	622	1 TBHU	thrombin (BC 3.4.2
9	90	47.1	482	1 EXRT	coagulation factor
10	90	47.1	617	2 S10511	thrombin (BC 3.4.2
11	88	46.1	458	2 A35827	thrombin (BC 3.4.2
12	88	46.1	465	1 KXBO	protein C (activat
13	86	45.0	475	1 EXCH	coagulation factor
14	81	42.4	461	1 KXHU	protein C (activat
15	78	40.8	416	1 KFB0	coagulation factor
16	77	40.3	461	1 KFHU	coagulation factor
17	74	38.7	625	1 TBBO	thrombin (BC 3.4.2
18	70	36.6	452	1 A30351	coagulation factor
19	70	36.6	452	1 UQ0419	coagulation factor
20	64	33.5	642	2 S53433	plasma protein S p
21	61	31.9	396	1 KXBO2	plasma protein Z -
22	60	31.4	675	1 KXBO5	plasma protein S p
23	59	30.9	642	2 S53434	plasma protein S p
24	59	30.9	642	1 KXHU5	plasma protein S p
25	58	30.4	646	2 S38819	plasma protein S p
26	57	29.8	675	1 KXRT5	plasma protein S p
27	56	29.3	422	1 KXHU2	plasma protein Z p
28	55.5	29.1	576	2 G96763	probable MAP kinase
29	50	26.2	673	2 A48089	growth arrest-spec

30	50	26.2	675	1 KXMS	plasma protein S p
31	49.5	25.9	594	2 D84859	probable MAP kinase
32	49.5	25.9	603	2 C96575	probable MAP kinase
33	48	25.1	674	2 I55476	growth potentialin
34	48	25.1	678	2 B48089	growth arrest-spec
35	45.5	23.8	83	2 T17839	hypothetical prote
36	45	23.6	271	2 S66691	hypothetical prote
37	45	23.6	879	2 S55864	hypothetical prote
38	45	23.6	907	2 T15792	hypothetical prote
39	44	23.0	306	2 T49068	protein kinase SRY
40	43.5	22.8	455	2 C83494	probable 2-isoprop
41	43	22.5	394	1 S30286	tetracycline resis
42	43	22.5	440	2 C70198	conserved hypothet
43	43	22.5	447	2 B95185	Mur ligase family
44	43	22.5	447	2 B98052	conserved hypothet
45	42.5	22.3	180	2 H90450	hypothetical prote

ALIGNMENTS

RESULT 1
KFHU7
coagulation factor VIIa (BC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII.
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:9180333; PID:AAA51963.1; PID:9180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3466420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M1323; NID:9182799; PID:AAA8040.1; PID:9182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <TH>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wiber, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A:Reference number: A40529; MUID:91250411; PMID:1904059
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: Protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:E7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1, 44/1, 97/3, 106/1, 144/1, 191/1, 227/3, 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-60/Domain: signal sequence #status predicted <PRO>
F/45-104/Domain: Gla domain homology <Gla>
F/61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F/110-141/Domain: EGF homology <EG1>
F/151-187/Domain: EGF homology <EG2>
F/213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F/213-466/Domain: trypsin homology <TRY>
F/66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F/177-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F/112,120/Binding site: carboxydrate (Ser) (covalent) #status experimental
F/123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F/205,382/Binding site: carboxydrate (Asn) (covalent) #status experimental
F/212-213/Cleavage site: Arg-11e (coagulation factor XIII) #status experimental
F/253,302,404/Active site: His, Asp, Ser #status predicted
F/350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.7%; Score 156; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 6,2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXXCSFXXAFIFKDXARTKLFWISY 44
61 ANAFLEELRPGSLERCKEELCSFEERAEIFKDXERTKLFWISY 104

RESULT 2
146932
Coagulation factor VII - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C/Accession: 146932
R/Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A/Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A/Reference number: 146932; MUID:93190306; PMID:8333365
A/Accession: 146932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-443 <BRO>
A/Cross-references: GB:S56300; NID:g266294; PID:g266295
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F/24-83/Domain: Gla domain homology <Gla>
F/89-120/Domain: EGF homology <EG1>
F/130-166/Domain: EGF homology <EG2>
F/192-425/Domain: trypsin homology <TRY>

Query Match 63.9%; Score 122; DB 2; Length 443;
Best Local Similarity 54.5%; Pred. No. 4,5e-13;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXXCSFXXAFIFKDXARTKLFWISY 44
40 ANSFLEELRPGSLERCKEELCSFEERAEVQSTERTKQFWITY 83

RESULT 3
KPB07
Coagulation factor VIIa (EC 3.4.21.21) - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C/Accession: A31979; C20274
R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A/Title: Bovine factor VII. Its purification and complete amino acid sequence.
A/Reference number: A31979; MUID:8908362; PMID:3049594
A/Accession: A31979
A/Molecule type: protein
A/Residues: 1-407 <TAK>
R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor
A/Reference number: A20274; MUID:83308813; PMID:6689526
A/Accession: C20274
A/Molecule type: protein
A/Residues: 58-62, 'X', 64-68 <MCM>
A/Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988
A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX
A/Reference number: A44556; MUID:89213999; PMID:3149637
A/Content: annotation
A/Note: structure and location of covalently bound carboxydrate
C/Function:
A/Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
A/Pathway: blood coagulation extrinsic pathway
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
F/1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F/1-44/Domain: Gla domain homology (fragment) <Gla>
F/50-81/Domain: EGF homology <EG1>
F/50-81/Domain: EGF homology <EG2>
F/51-127/Domain: EGF homology <EG3>
F/153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F/153-407/Domain: trypsin homology <TRY>
F/66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F/177-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F/112,120/Binding site: carboxydrate (Ser) (covalent) #status experimental
F/123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F/205,382/Binding site: carboxydrate (Asn) (covalent) #status experimental
F/212-213/Cleavage site: Arg-11e (coagulation factor XIII) #status experimental
F/253,302,404/Active site: His, Asp, Ser #status predicted
F/350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 59.7%; Score 114; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 1e-11;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXXCSFXXAFIFKDXARTKLFWISY 44
Db 1 ANSFLEELRPGSLERCKEELCSFEERAEVQSTERTKQFWISY 44

RESULT 4
JX0210
Protein C (activated) (EC 3.4.21.69) precursor - mouse
N/Alternate names: vitamin K-dependent serine proteinase
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JX0210
R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A/Title: Isolation and characterization of a mouse protein C cDNA.
A/Reference number: JX0210; MUID:92316897; PMID:1618739
A/Accession: JX0210
A/Molecule type: mRNA
A/Residues: 1-461 <TAD>
A/Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
A/Experimental source: liver
C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that r

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
F/1-33/Domain: signal sequence #status predicted <SIG>
F/27-85/Domain: Gla domain homology <Gla>
F/34-41/Domain: propeptide #status predicted <PRO>
F/42-196,199-461/Product: protein C #status predicted <PCL>
F/42-196/Domain: light chain #status predicted <PCL>
F/91-130/Domain: EGF homology <EG1>
F/139-174/Domain: EGF homology <EG2>
F/199-461/Domain: heavy chain #status predicted <PCH>
F/199-211/Domain: activation peptide #status predicted <ACT>
F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

U. Mol. Biol. 222, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A/Reference number: A49458; PMID:93360277; PMID:8355279
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T>
 A/Note: The two chains held together by one disulfide bond are formed from a single-c
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C/Genetics:
 A/Gene: GDB:P10
 A/Cross-references: GDB:119890; OMIM:227600
 A/Map position: 13q34-13q34
 A/Intons: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A/Note: deficiency of this factor causes Stuart disease
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-40/Domain: propeptide #status predicted <PRO>
 F/25-94/Domain: Gla domain homology <GLA>
 F/90-121/Domain: EGF homology <EG1>
 F/129-164/Domain: EGF homology <EG2>
 F/183-488/Domain: coagulation factor X heavy chain #status experimental <LCH>
 F/233-488/Domain: activation peptide #status experimental <ACT>
 F/235-488/Domain: coagulation factor Xa heavy chain #status experimental <ACT>
 F/235-462/Domain: trypsin homology <TRY>
 F/46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F/57-62/Disulfide bonds: #status predicted
 F/80-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F/199, 211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F/221, 231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F/234-235/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat
 F/276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.3%; Score 96; DB 1; Length 488;
 Best Local Similarity 38.6%; Pred. No. 1.5e-08;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLREGSLRXCCKXCFXAFKFXKXRTKLFMTSY 44
 41 ANSFLBEMKCHLRBCEMERTCSYBAREVEDSDKTFPNKX 84

RESULT 7
 EXBO
 coagulation factor Xa (BC 3.4.21.6) precursor - bovine
 N/Alternate names: Stuart factor (cattle)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text change 16-Jul-1999
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 F/Fung: M.R.; Campbell, R.M.; MacGillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A/Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A/Reference number: A22867; PMID:8424315; PMID:6330671
 A/Accession: A22867
 A/Molecule type: mRNA
 A/Residues: 1-487 <FNU>
 A/Cross-references: GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
 B/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A/Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A/Reference number: A14997; PMID:80130563; PMID:6766735
 A/Accession: A14997
 A/Molecule type: protein
 A/Residues: 41-102, 'N', 104-180 <EN>
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A/Reference number: A20274; PMID:83308813; PMID:6688526
 A/Contents: annotation; revision to residue 103
 R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A/Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A/Reference number: A12030; PMID:76053069; PMID:1059093
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T>
 A/Note: carboxylate binding sites and disulfide bonds were determined
 R/Persson, E.; Selander, M.; Linn, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.
 U. Biol. Chem. 264, 16897-1694, 1989
 A/Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A/Reference number: A34412; PMID:89380326; PMID:2789221
 A/Accession: A34412
 A/Molecule type: protein
 A/Residues: 65-126 <PER>
 A/Note: beta-hydroxyaspartic acid site
 R/Imoue, K.; Morita, T.
 Eur. J. Biochem. 210, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; PMID:94062825; PMID:8243461
 A/Accession: S39414
 A/Molecule type: protein
 A/Residues: 183-196,199-209,216-233 <INO>
 A/Note: carboxylate binding sites
 R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A/Title: Bovine factor X-1a (activated Stuart factor): Evidence of homology with mammali
 A/Reference number: A12453; PMID:73053314; PMID:466486
 A/Contents: annotation; active site
 R/Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A/Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
 A/Reference number: A13504; PMID:76053121; PMID:1059122
 A/Contents: annotation; activation
 R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A/Reference number: A38024; PMID:84185716; PMID:6546930
 A/Contents: annotation; calcium binding
 R/Morita, T.; Jackson, C.W.
 J. Biol. Chem. 261, 4008-4014, 1986
 A/Reference number: A38025; PMID:86140210; PMID:3949800
 A/Contents: annotation; sulfate binding
 C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
 C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamir
 C/Genetics:
 A/Gene: F10
 A/Map position: 13q34
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
 F/1-15/Domain: signal sequence #status predicted <SIG>
 F/16-40/Domain: propeptide #status predicted <PRO>
 F/25-84/Domain: Gla domain homology <GLA>
 F/41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F/90-121/Domain: EGF homology <EG1>
 F/129-164/Domain: EGF homology <EG2>
 F/183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F/233-492/Domain: activation peptide #status experimental <APT>
 F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F/234-461/Domain: trypsin homology <TRY>
 F/46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #
 F/57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status
 F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F/200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F/208, 485/Binding site: carboxylate (Thr) (covalent) #status experimental
 F/218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F/233-234/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat

C:Accession: A26250; A18385; A18386; A00928
 R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
 A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
 A:Reference number: A26250; MUID:85014826; PMID:6091100
 A:Accession: A26250
 A:Molecule type: mRNA
 A:Residues: 1-456 <LRN>
 R:Fernlund, P.; Stenflo, J.
 J. Biol. Chem. 257, 12170-12179, 1982
 A:Title: Amino acid sequence of the light chain of bovine protein C.
 A:Reference number: A18385; MUID:83007325; PMID:6896876
 A:Accession: A18385
 A:Molecule type: protein
 A:Residues: 40-194 <FER>
 A>Note: 82-Lys was also found
 R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
 A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A:Reference number: A19316; MUID:83169769; PMID:6572339
 A:Accession: A19316
 A:Content: annotation; revision to residue 110
 R:Stenflo, J.; Fernlund, P.
 J. Biol. Chem. 257, 12180-12190, 1982
 A:Title: Amino acid sequence of the heavy chain of bovine protein C.
 A:Reference number: A18386; MUID:83007326; PMID:6896877
 A:Accession: A18386
 A:Molecule type: protein
 A:Residues: 197-454, 'PV' <STE>
 R:Esmon, N.L.; DeBaillie, L.E.; Esmon, C.T.
 J. Biol. Chem. 258, 5548-5553, 1983
 A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless P
 A:Reference number: A37541; MUID:83213513; PMID:6304092
 A:Accession: A37541
 A:Content: annotation; activation; calcium binding
 R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.
 J. Biol. Chem. 258, 5554-5560, 1983
 A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin
 A:Reference number: A37542; MUID:83213514; PMID:6406503
 A:Accession: A37542
 A:Content: annotation; activation; calcium binding
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
 B.
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 cogitation of the thrombin-thrombomodulin complex.
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
 F:24-83/Domain: Gla domain homology <GLA>
 F:30-39/Domain: propeptide #status predicted <PRO>
 F:40-194/Product: protein C light chain #status experimental <LCH>
 F:98-128/Domain: EGF homology <EG1>
 F:137-172/Domain: EGF homology <EG2>
 F:197-456/Product: protein C heavy chain #status experimental <HCH>
 F:197-210/Domain: activation peptide #status experimental <APT>
 F:211-440/Domain: trypsin homology <TRY>
 F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:110/Modified site: ethylro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:116,128,137-148,144-157,159-172,180-194,237-253,366-382,393-421/Disulfide bonds: #stab
 F:152,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:252,298,397/Active site: His, Asp, Ser #status predicted
 F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.1%; Score 88; DB 1; Length 456;
 Best Local Similarity 40.9%; Pred. No. 3.5e-07;
 Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFXXLRBGSIXRCXKXQCSFXXAFIFKDXARTKLFWISY 44
 DB 40 ANSFLEELRPGNVERECSEVCEFEAREIFONTEDTMAWSPY 83

RESULT 13

EXCH
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken
 N:Alternate names: virus-activating proteinase
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
 C:Accession: S15838; S20380; S20381
 R:Suzuki, H.; Harada, A.; Hayaishi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
 FEBS Lett. 283, 281-285, 1991
 A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
 A:Reference number: S15838; MUID:91257322; PMID:2044767
 A:Accession: S15838
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-475 <SUZ>
 A:Cross-references: DDBJ:00844; NID:9222869; PIDN:BA00724.1; PID:9222870
 R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
 FEBS Lett. 296, 274-278, 1992
 A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
 A:Reference number: S20380; MUID:92164779; PMID:1537403
 A:Accession: S20380
 A:Molecule type: protein
 A:Residues: 41-55 <GOT>
 A:Accession: S20381
 A:Molecule type: protein
 A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:81-185/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-167/Domain: EGF homology <EG2>
 F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:186-240/Domain: activation peptide #status predicted <APT>
 F:241-475/Product: coagulation factor Xa heavy chain #status experimental <HCH>
 F:241-468/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,70-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42
 F:103/Modified site: ethylro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 45.0%; Score 86; DB 1; Length 475;
 Best Local Similarity 36.4%; Pred. No. 8e-07;
 Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFXXLRBGSIXRCXKXQCSFXXAFIFKDXARTKLFWISY 44
 DB 41 ANSFLEEMKQNIERNERNBCSKSEAREAFEDNEXTEBSFWNLY 84

RESULT 14

protein C (activated) (EC 3.4.21.6) precursor - human
 N:Alternate names: autoprothrombin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Forster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A:Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOR>
 A:Cross-references: GB:M1228; NID:9190333; PIDN:AAA60166.1; PID:9190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A:Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471
 A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445; 'L', 446-461 <PU>
 A:Cross-references: GB:M1212; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Poster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'Q', 107-461 <FOS2>
 A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Miletic, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation
 A:Reference number: A44605; MUID:90293094; PMID:1694179
 A:Ccontents: annotation; carbohydrate binding sites; activation peptide
 A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 J.Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544894
 A:Ccontents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 ulation of factor Va is strongly enhanced by complexing with protein S. Protein C also
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Insertions: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <Gla>
 F:43-197/Product: protein C light chain #status predicted <PRO>
 F:92-131/Domain: EGF homology <EGF>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <HC>
 F:200-211/Domain: activation peptide #status experimental <AP1>
 F:212-445/Domain: trypsin homology <TRY>
 F:49-56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

```

coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #ext:change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Tr
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
A:Reference number: A14757; PMID:80056619; PMID:251916
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', 65-416 <RAT>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood cc
A:Reference number: A20274; PMID:83308813; PMID:6685526
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', 65-69 <MCM>
R:Choo, K.H.; Gould, K.G.; Reese, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; PMID:82272386; PMID:6287289
A:Accession: I45891
A>Status: translated from GB/EMBL/DBSJ
A:Molecule type: mRNA
A:Residues: 52-139 <CHO>
A:Cross-references: GB:J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
R:Haee, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa
A:Reference number: A44556; PMID:89213999; PMID:3149657
A:Contents: annotation
A>Note: structure and location of a carbohydrate covalently bound to Ser
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide p
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stru
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pres
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxygluta
F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <GLA>
F:51-82/Domain: EGF homology <EG1>
F:88-124/Domain: EGF homology <EG2>
F:147-181/Domain: activation peptide #status experimental <APT>
F:188-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:188-409/Domain: trypsin homology <TRY>
F:17-8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #st
F:18-23,51-62,56-11,73-82,88-99,99-109,111-124,132-290,207-223,337-351,362-390/Dsulfid
F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 40.8%; Score 78; DB 1; Length 416;
Best Local Similarity 41.2%; Pred. No. 1,7e-05;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLRXCKXKOCSEFXAXFKADARTLPIISY 44
DB 12 GNLERCKEBKCSFEAREVEENTKTEFWKQY 45

Search completed: March 19, 2003, 15:00:51
Job time : 30.125 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFLLXLRGSLXRXCKX.....XXAFIFDXARTKLFMISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	FA7_HUMAN	P08709 homo sapien
2	122	63.9	444	FA7_RABIT	P98139 oryctolagus
3	114	59.7	407	FA7_BOVIN	P22457 bos taurus
4	111	58.1	446	FA7_MOUSE	P10945 mus musculu
5	102	53.4	490	FA10_RABIT	O19045 oryctolagus
6	98	51.3	459	PRTC_PIG	O991P2 sus scrofa
7	97	50.8	461	PRTC_MOUSE	P33587 mus musculu
8	96	50.3	488	PRTC_RAT	P00742 homo sapien
9	96	50.3	488	FA10_HUMAN	P00743 bos taurus
10	96	50.3	492	FA10_HUMAN	O14668 homo sapien
11	94	49.2	218	THRB_HUMAN	P00734 homo sapien
12	94	49.2	622	THRB_HUMAN	P18292 rattus norv
13	90	47.1	617	THRB_RAT	P19221 mus musculu
14	88	46.1	456	PRTC_MOUSE	P00745 bos taurus
15	88	46.1	456	PRTC_BOVIN	O991P2 sus scrofa
16	86	45.0	231	FA10_HUMAN	P25155 gallus gall
17	86	45.0	475	FA10_CHICK	O28661 oryctolagus
18	81	42.4	458	PRTC_RABIT	P04070 homo sapien
19	81	42.4	461	PRTC_HUMAN	P00741 bos taurus
20	78	40.8	416	FA9_BOVIN	P00740 homo sapien
21	77	40.3	461	FA9_HUMAN	P81428 tropidochis
22	76	39.8	376	FA10_TROCA	P00735 bos taurus
23	74	38.7	625	THRB_BOVIN	O14669 homo sapien
24	73	38.2	202	THRB_HUMAN	P18292 rattus norv
25	70	36.6	452	FA9_MOUSE	P16294 mus musculu
26	70	36.6	459	FA9_MOUSE	O991P2 sus scrofa
27	66.5	34.8	226	TMG4_HUMAN	P00744 bos taurus
28	61	31.9	396	PRTC_BOVIN	P07224 bos taurus
29	60	31.4	675	PRTC_BOVIN	O28620 macaca mula
30	59	30.9	649	PRTC_MACMO	P98118 oryctolagus
31	59	30.9	649	PRTC_HUMAN	P55813 rattus norv
32	58	30.4	646	PRTC_RABIT	
33	57	29.8	675	PRTC_RAT	

34	56	29.3	400	1	PRTC_HUMAN	P22891 homo sapien
35	50	26.2	675	1	PRTC_MOUSE	O08761 mus musculu
36	45	23.6	271	1	MD12_YEAST	O92328 saccharomyc
37	45	23.6	879	1	YN65_YEAST	P42831 saccharomyc
38	43	22.5	343	1	HMD_METVO	O50840 methanococc
39	43	22.5	353	1	HMD_METTL	O50759 m coenzyme
40	43	22.5	394	1	TCR4_SALOR	P33733 salmoneilla
41	43	22.5	440	1	Y788_BORBU	O51728 borreliella bu
42	42	22.0	185	1	HEX1_MOUSE	O61658 mus musculu
43	41	21.5	263	1	PLIA_STRMU	O68575 streptococc
44	41	21.5	393	1	DP85_PINSY	O02323 pinus sylve
45	41	21.5	616	1	JEN1_YEAST	P36035 saccharomyc

ALIGNMENTS

RESULT 1
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; O14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Liver;
RC MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.",
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.",
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.",
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.",
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN
 RP
 RX STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN
 RP
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN
 RP
 RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN
 RP
 RX STRUCTURE BY NMR OF 105-145
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gispert G.P., Forssen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN
 RP
 RX VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN
 RP
 RX VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN
 RP
 RX VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN
 RP
 RX VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Pelten A., Mellis E., Hahn I., Prangnell D.R., Lunley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN
 RP
 RX VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chabot S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN
 RP
 RX VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN
 RP
 RX VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN
 RP
 RX VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Abidin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr399Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN
 RP
 RX VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN
 RP
 RX VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligson U.;
 RT "Val244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN
 RP
 RX VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN
 RP
 RX -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSES. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -I- TISSUE SPECIFICITY: PLASMA.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -I- PHARMACEUTICAL: Available under the names Nistase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 81.7%; Score 156; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 7.2e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

1 ANAFLXLRGSLRXCKXQCSFXAXFIPKDAKRTKLFWISY 44
61 ANAFLELRPGSLERCKECSFEARERIFKDAERTKLFWISY 104

RESULT 2

FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brocheys A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RT Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruit S.R., Blajchman M.A., Clarke B.J.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U77477; AAB37326.1; -.
DR HSSP; P08709; 1FAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Sec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 363 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 63.9%; Score 122; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 7.1e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

1 ANAFLXLRGSLRXCKXQCSFXAXFIPKDAKRTKLFWISY 44
40 ANAFLELRPGSLERCKECSFEARERFPOSTERTKOFWITY 83

RESULT 3

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FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
  accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovidae; Bovine; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
  Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
  Iwanaga S.,
  "Bovine factor VII. Its purification and complete amino acid
  sequence."
  J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
  Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
  Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
  "A new trisaccharide sugar chain linked to a serine residue in bovine
  blood coagulation factors VII and IX."
  J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=9134709; PubMed=2129367;
  Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
  "A new trisaccharide sugar chain linked to a serine residue in the
  first EGF-like domain of clotting factors VII and IX and protein Z."
  Adv. Exp. Med. Biol. 281:121-131(1990).
CC - FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
  CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
  THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
  AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
  BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
  FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC - CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
  form factor Xa.
CC - SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
  BY A DISULFIDE BOND.
CC - TISSUE SPECIFICITY: PLASMA.
CC - PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
  GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
  CALCIUM.
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; -.
DR InterPro: IPR000152; Aex_hydroxy1.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_T1.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.

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DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
  KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
  EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT SITE 193 193
FT ACT SITE 242 242
FT ACT SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 92 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 7
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 70351F0636F7F10 CRC64;

Query Match 59.7%; Score 114; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 1,7e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANAFLLXLRBESLXRKXKXQCSFYXAFIKDAXRKLFLFISY 44
Db 1 ANGFLBLLPGLSERECREBLCSFEAEHLFRNEERTQFVWSY 44

RESULT 4
FA7_MOUSE STANDARD; PRT; 446 AA.
ID FA7_MOUSE
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
  conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RX Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@sib.ch).
 CC -----
 CC EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BR9.
 DR MEROPS; S01.215; -.
 DR MCD; MGI:109325; F7.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SMO0179; EGF_CA; 1.
 DR SMART; SMO0001; EGF_like; 1.
 DR SMART; SMO0069; GLA; 1.
 DR SMART; SMO0020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SBR; 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41 POTENTIAL.
 FT CHAIN 42 193 FACTOR VII LIGHT CHAIN.
 FT CHAIN 194 446 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 47 76 GLA-RICH.
 FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 128 169 EGF-LIKE 2.
 FT DOMAIN 194 446 SERINE PROTEASE.
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,
 FT ACT_SITE 234 234 FACTOR IXa OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT ACT_SITE 385 385 BY SIMILARITY.
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 113 122 BY SIMILARITY.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 139 153 BY SIMILARITY.
 FT DISULFID 155 168 BY SIMILARITY.
 FT DISULFID 176 303 BY SIMILARITY.
 FT DISULFID 200 205 BY SIMILARITY.
 FT DISULFID 219 235 BY SIMILARITY.
 FT DISULFID 351 370 BY SIMILARITY.
 FT DISULFID 381 409 BY SIMILARITY.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 446 AA; 50276 MW; 2512B44A5CB96E CRC64;
 Query Match 58.1%; Score 111; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 6.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ANAFLLXIREGSLKXKCKXKQCSFXXAKYIFDAXRTKLFWISY 44
 DB 42 ANSLLEELWPGSLREBCEQCSEFEAREIFSPRTKQFWIVY 85
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X."
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC strongly promoted by thrombomodulin.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the Gla domain. This Gla-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF191307; AAG28380.1; --
 CC HSSP: P04070; 1PCU.
 CC MEROPS: S01.218; --
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TYP_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_SRS; 1.
 DR PROSITE: PS00135; TRYPSIN_SRS; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61

FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 51.3%; Score 98; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 1.3e-09;
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANAFLLXLESGSLRXCKXKCSFKXAFIFKDAKRTKLFWSY 44
 DB 42 ANSFLELRPSLSRCKERTCFEAREIFONTENTYAFWSKY 85
 RESULT 7
 ID_PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tawjima A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jaldert L.R., Rosen B.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

```

RT      "A comparative study of partial primary structures of the catalytic
RT      region of mammalian protein C".
RL      Br. J. Haematol. 86:590-600(1994).
CC      -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC      REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC      IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC      -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC      and VIIIA.
CC      -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC      INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC      BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC      TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC      REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC      STRONGLY PROMOTED BY THROMBOMODULIN.
CC      -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.
CC      -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC      GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC      -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC      ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC      SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC      THROMBIN-THROMBOMODULIN COMPLEX.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC      -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.lab-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; D10445; BAA01235.1; -.
DR      EMBL; AF034569; AAC3795.1; -.
DR      EMBL; D43755; BAA07812.1; -.
DR      PIR; JX0210; JX0210.
DR      HSSP; P04070; 1PCU.
DR      MEROPS; S01.218; -.
DR      MOD; MGI:97771; Piroc.
DR      InterPro: IPR000152; Axx_hydroxyl.
DR      InterPro: IPR001314; Chymotrypsin.
DR      InterPro: IPR000561; EGF-like.
DR      InterPro: IPR001881; EGF Ca.
DR      InterPro: IPR002383; GLA_Blood.
DR      InterPro: IPR001254; Ser_protease_Ty.
DR      InterPro: IPR000294; VitK_dep_GLA.
DR      Pfam; PF00008; EGF; 2.
DR      Pfam; PF00089; trypsin; 1.
DR      Pfam; PF00594; glaf; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      PRINTS; PR00001; GLABLOOD.
DR      SMART; SM00179; EGF_CA; 1.
DR      SMART; SM00001; EGF_like; 1.
DR      SMART; SM00069; GLA; 1.
DR      SMART; SM00020; TRYR_SPC; 1.
DR      PROSITE; PS00010; ASX_HYDROXYL; 1.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 2.
DR      PROSITE; PS01187; EGF_CA; 1.
DR      PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR      PROSITE; PS00240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
DR      Blood coagulation; Glycoprotein; Serine protease;
DR      Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM      EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT      STGNL      1      33
FT      PROPEP      34      41
FT      CHAIN      42      196
FT      CHAIN      199      461
FT      PEPTIDE      199      212
FT      SITE      212      213
FT      DOMAIN      96      131

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FT      DOMAIN      135      175
FT      MOD_RES      213      461
FT      MOD_RES      47      47
FT      MOD_RES      48      48
FT      MOD_RES      55      55
FT      MOD_RES      57      57
FT      MOD_RES      60      60
FT      MOD_RES      61      61
FT      MOD_RES      66      66
FT      MOD_RES      67      67
FT      MOD_RES      70      70
FT      MOD_RES      112      112
FT      ACT_SITE      253      253
FT      ACT_SITE      299      299
FT      ACT_SITE      402      402
FT      DISULFID      58      63
FT      DISULFID      91      110
FT      DISULFID      100      105
FT      DISULFID      104      119
FT      DISULFID      121      130
FT      DISULFID      139      150
FT      DISULFID      146      159
FT      DISULFID      161      174
FT      DISULFID      182      319
FT      DISULFID      238      254
FT      DISULFID      373      387
FT      DISULFID      398      426
FT      CARBOHYD      214      214
FT      CARBOHYD      290      290
FT      CARBOHYD      355      355
FT      CONFLICT      328      328
FT      CONFLICT      393      393
SQ      SEQUENCE      461 AA; 51945 MW; 53FA0D85B194D6E CRC64;

Query Match      50.8%; Score 97; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.9e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Cy      1 ANAFLLXLRREGSLKRCCKXXQCSFXAFLFKDAXRTKFLWISY 44
Db      42 ANSLFEMRPGSLERECMEICDFEERAGELFQNVEDTLAWIKY 85

RESULT 8
PRTC RAT      STANDARD; PRT; 461 AA.
AC      P1354;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE      (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
DE      factor XIV).
GN      PROC.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
ON      [1]
AP      SEQUENCE FROM N.A.
AP      STRAIN=Wistar; TISSUE=Liver;
RX      MEDLINE=92329550; PubMed=1627650;
RA      Okafor T., Maekawa K., Nawa K., Marumoto Y.;
RT      "The cDNA cloning and mRNA expression of rat protein C.";

```


RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 blood coagulation factor X.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RX TISSUE=Liver;
 RC MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 cDNA.";
 RT Gene 41:311-314(1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kisiel W., Saegawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 coagulation factor X: evidence for identification of residue 63 as
 beta-hydroxyaspartic acid.";
 RT Biochemistry 22:2875-2884(1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:3659-3702(1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 peptides of blood coagulation factor X. The role of the carbohydrate
 moieties in the activation of factor X.";
 RT Eur. J. Biochem. 218:153-163(1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=9012829; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamzahsham K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon I) of the gene
 encoding human factor X.";
 RT Gene 84:517-519(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RT J. Mol. Biol. 232:947-966(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 factor Xa.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 RN [11]
 RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 converts prothrombin to thrombin in the presence of factor Va,
 calcium and phospholipid during blood clotting.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 Arg-|-Ile bonds in prothrombin to form thrombin.
 CC SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 MORE DISULFIDE BONDS.
 CC TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM.

CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, K03194; AAA52490.1; -
 DR EMBL, M57285; AAA52421.1; -
 DR EMBL, L29433; AAA52764.1; -
 DR EMBL, L00390; AAA52764.1; JOINED.
 DR EMBL, L00391; AAA52764.1; JOINED.
 DR EMBL, L00392; AAA52764.1; JOINED.
 DR EMBL, L00393; AAA52764.1; JOINED.
 DR EMBL, L00394; AAA52764.1; JOINED.
 DR EMBL, L00395; AAA52764.1; JOINED.
 DR EMBL, L00396; AAA52764.1; JOINED.
 DR EMBL, M22613; AAA51984.1; -
 DR EMBL, K01886; AAA52486.1; -
 DR EMBL, M33297; AAA52636.1; -
 DR PIR, A00924; EXHU.
 DR PIR, A25853; A25853.
 DR PIR, A24478; A24478.
 DR PDB, 1HCG; 08-MAY-95.
 DR PDB, 1FAK; 29-OCT-97.
 DR PDB, 1EXY; 17-JUN-98.
 DR PDB, 1XKA; 23-MAR-99.
 DR PDB, 1XXB; 23-MAR-99.
 DR MEROPS, S01.216; -
 DR GLYCOsiteDB; P00742; -
 DR Genew, HGNC:3528; F10.
 DR MIM, 134530; -
 DR MIM, 227600; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF_1-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00089; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00594; gla_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00061; EGF_1like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein, Hydrolase, Serine protease; Plasma, blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL; 1; 31; POTENTIAL.
 FT PROPEP; 32; 40; FACTOR X LIGHT CHAIN.
 FT CHAIN; 41; 179; FACTOR X HEAVY CHAIN.
 FT CHAIN; 183; 488; ACTIVATION PEPTIDE.
 FT PROPEP; 183; 234;


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FT CHAIN 235 488 ACTIVATED FACTOR Xa, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013. . .).
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

Query Match 50.3%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 3.1e-09;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFKXLRGSLKRYCKXQCSFXXAFKFKDARTKLFWISY 44
Db 41 ANSFLEMKKGLHRECMETCSYEAREVFEDSDKTFNFMKY 84

RESULT 10
ID FA10 BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin

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RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053114; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teleman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sumnerhagen M., Ullner M., Persson E., Teleman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";

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DR Pfam: PF00594; gls; 1.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SMO0069; GLA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1. Transmembrane.
 KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 FT PROPEP 1 20
 FT CHAIN 21 218
 FT DOMAIN 21 83
 FT TRANSMEM 84 106
 FT DOMAIN 107 218
 FT DOMAIN 24 61
 FT DOMAIN 131 135
 FT POLY-PRO.
 FT SEQUENCE 218 AA; 24947 MW; 26538A61A0A0EB98 CRC64;
 Query Match 49.2%; Score 94; DB 1; Length 218;
 Best Local Similarity 38.6%; Pred. No. 3.2e-09;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Db 1 ANAFLLXRLREGSLRXCKKXQCSFXXAFXFQXAXRTKLFWISY 44
 21 ANGFEEIRKGNIERECKERCTFEAREAFENNEKTEKFWSTY 64

RESULT 12
 THRB HUMAN STANDARD; PRT; 622 AA.
 AC P00734;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5) (coagulation factor II).
 GN F2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8077877; PubMed=2825773;
 RA Degen S.J.F., Davie E.W.;
 RT "Nucleotide sequence of the gene for human prothrombin.";
 RL Biochemistry 26:6165-6177(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT MET-165.
 RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBD databases.
 RN [3]
 RP SEQUENCE OF 8-622 FROM N.A.
 RX MEDLINE=8331469; PubMed=6305407;
 RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of the complementary deoxyribonucleic acid and gene
 coding for human prothrombin.";
 RL Biochemistry 22:2087-2097(1983).
 RN [4]
 RP SEQUENCE OF 44-314.
 RX MEDLINE=77193964; PubMed=266717;
 RA Walz D.A., Hewett-Emmett D., Seegers W.H.;
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
 RN [5]
 RP SEQUENCE OF 315-622.
 RX MEDLINE=77207112; PubMed=873923;
 RA Butkewski R.J., Elion J., Downing M.R., Mann K.G.;
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
 RL J. Biol. Chem. 252:4942-4957(1977).
 RN [6]
 RP PROCESSING.
 RX MEDLINE=87008532; PubMed=3759958;
 RA Rabiet M.J., Blaschill A., Furie B., Furie B.C.;
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
 activation in human plasma.";

RL J. Biol. Chem. 261:13210-13215(1986).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=90059942; PubMed=2583108;
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
 RT "The refined 1.9 A crystal structure of human alpha-thrombin:
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of
 the Tyr-Pro-Pro-Trp insertion segment.";
 RL EMBO J. 8:3467-3475(1989).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=90327074; PubMed=2374926;
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Roitsch C., Fenton J.W. II;
 RT "The structure of a complex of recombinant hirudin and human alpha-
 thrombin.";
 RL Science 249:277-280(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94350942; PubMed=8071320;
 RA Rydel T.J., Yin W., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin.";
 RL J. Biol. Chem. 269:22000-22006(1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=97357286; PubMed=9214615;
 RA van de Locht A., Bode W., Huber R., Je Bonniec B.F., Stone S.R.,
 RA Esmen C.T., Stubbs M.T.;
 RT "The thrombin E192Q-BPTI complex reveals gross structural
 rearrangements: implications for the interaction with antithrombin
 and thrombomodulin.";
 RL EMBO J. 16:2977-2984(1997).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
 RX MEDLINE=99162521; PubMed=10051558;
 RA Guineto E.R., Caccia S., Rose T., Fueterer K., Wakeman G., di Cera E.;
 RT "Unexpected crucial role of residue 225 in serine proteases";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 RN [12]
 RP VARIANT BARCELONA.
 RX MEDLINE=87033739; PubMed=3771562;
 RA Rabiet M.-J., Furie B.C., Furie B.;
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
 for arginine at residue 273.";
 RL J. Biol. Chem. 261:15045-15048(1986).
 RN [13]
 RP VARIANT FRANKFURT.
 RX MEDLINE=95313001; PubMed=7792730;
 RA Degen S.J.F., McDowell S.A., Sparks L.W., Scharrer I.;
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
 substitution of Glu-466 by Ala.";
 RL Thromb. Haemost. 73:203-209(1995).
 RN [14]
 RP VARIANTS HIMI-1 AND HIMI-2.
 RX MEDLINE=93043342; PubMed=1421398;
 RA Morishita E., Saio M., Kumabashiri I., Asakura H., Matsuda T.,
 RA Yamaguchi K.;
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
 prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
 RL Blood 80:2275-2280(1992).
 RN [15]
 RP VARIANT PADUA-1.
 RX MEDLINE=95169898; PubMed=7865694;
 RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
 RT "Prothrombin Padua I: incomplete activation due to an amino acid
 substitution at a factor Xa cleavage site.";
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).
 RN [16]
 RP VARIANT QUITK-1.
 RX MEDLINE=89207504; PubMed=3242619;
 RA Henriksen R.A., Mann K.G.;
 RT "Identification of the primary structural defect in the dysfibrinogen

```

CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
CC NATURAL BLOOD CLOTTING.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-199, OBSERVED IN VITRO, DOES
CC
CC Query Match 49.2%; Score 94; DB 1; Length 622;
CC Best Local Similarity 38.6%; Pred. No. 8.9e-09;
CC Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
CC
Cc 1 ANAFXXLRREGSLKRXCKXXCSPFXAXFXIKDXKRTLEFWISY 44
Cc |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Cc 44 ANTFLEVRKGNLERECVEETCTSYEAFALESSTADIVFWAKY 87
Cc
Cc RESULT 13
Cc ID_THRB_RAT STANDARD; PRT; 617 AA.
Cc AC P18292;
Cc DT 01-NOV-1990 (Rel. 16, Created)
Cc DT 01-NOV-1990 (Rel. 16, Last sequence update)
Cc DT 15-JUN-2002 (Rel. 41, Last annotation update)
Cc DE Prothrombin precursor (EC 3.4.21.5).
Cc GS P2.
Cc OS Rattus norvegicus (Rat).
Cc OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Cc OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
Cc CX NCBI_TaxID=10116;
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Cc SEQUENCE FROM N.A.
Cc RP STRAIN=Sprague-Dawley; TISSUE=Liver;
Cc RX MEDLINE=90332426; PubMed=2377469;
Cc RA Dhanich M., Monard D.;
Cc RT "cDNA sequence of rat prothrombin.";
Cc RL Nucleic Acids Res. 18:4251-4251(1990).
Cc [2]
Cc SEQUENCE OF 383-617 FROM N.A.
Cc RP TISSUE=Liver;
Cc RX MEDLINE=92212913; PubMed=1557383;
Cc RA Banfield D.K., Macgillivray R.T.;
Cc RT "Partial characterization of vertebrate prothrombin cDNAs:
Cc RT amplification and sequence analysis of the B chain of thrombin from
Cc RT nine different species.";
Cc RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
Cc -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
Cc FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
Cc AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,
Cc -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
Cc fibrinogen to fibrin and releases fibrinopeptide A and B.
Cc -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
Cc RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
Cc ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
Cc ARE NECESSARY FOR THE Ca-DEPENDENT INTERACTION WITH A NEGATIVELY
Cc CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
Cc OF PROTHROMBIN TO THROMBIN.
Cc -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
Cc PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
Cc FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
Cc THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
Cc HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
Cc V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
Cc THROMBIN.
Cc -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
Cc FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
Cc BY FACTOR XA.
Cc -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
Cc -1- SIMILARITY: CONTAINS 2 KRINGE DOMAINS.
Cc -----
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EMBL; X52835; CA37017.1; -
EMBL; M81397; AAA4240.1; -
PIR; S10511; S10511.
HSSP; P00734; 1UVS.
MEROPS; S01.217; -
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR000294; VicK_dep_GLA.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; TRY-SPC; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS00070; KRINGLE_2; 2.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Hydroxylase; Serine protease; Kringle; Signal.
KMW SIGNAL. 1 24
PROPEP 25 43
CHAIN 44 617
PEPTIDE 200
PEPTIDE 201 323
CHAIN 324 359
CHAIN 360 617
DOMAIN 109 187
DOMAIN 215 292
DOMAIN 360 617
SITE 200 201
SITE 323 324
SITE 359 360
ACT_SITE 402 402
ACT_SITE 458 458
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MOD_RES 50 50
MOD_RES 51 51
MOD_RES 58 58
MOD_RES 60 60
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MOD_RES 69 69
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MOD_RES 73 73
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CARBOHYD 120 120
CARBOHYD 144 144
CARBOHYD 412 412
CARBOHYD 552 552
DISULFID 61 66
DISULFID 91 104
DISULFID 109 187
DISULFID 130 170
DISULFID 158 182
DISULFID 215 292
DISULFID 236 276

FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
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FT DISULFID 560 590 BY SIMILARITY.
SQ SEQUENCE 617 AA; 70411 MW; AD27D1B71450B1D CRC64;
Query Match 47.1%; Score 90; DB 1; Length 617;
Best Local Similarity 39.5%; Pred. No. 4.5e-08;
Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 2 MAFLLXLRGSLKXCKXXQCSPXAFIFKAKRTKLFWIST 44
DB 46 SGFLIELRKGNLERCEVEECQSYEEAFEALESFQDTVFWAKY 88
RESULT 14
THRB_MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (BC 3.4.21.5).
GN F2 OR CP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=9102551; PubMed=2222810;
RA Fritzenner Degen S.O., Schaffer L.A., Jamison C.S., Grant S.G., Fitzgibbon J.V., Bai J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-496(1990).
RN [2]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Gly, activates fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).

DR EMBL: X52308; CAA36548.1; -
 DR EMBL: M81394; AAA40435.1; -
 DR PIR: A35827; A35827.
 DR HSSP: P00734; 187X.
 DR MEROPS: S01.217; -
 DR MGD: MGI:88380; F2.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00051; kringle_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle_2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRY_PPC; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 KM Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 KM Hydrolyase; Serine protease; Kringle; Signal.
 KM SIGNAL 1 24
 FT PROPEP 25 43
 FT CHAIN 44 618
 FT PEPTIDE 44 200
 FT PEPTIDE 201 324
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 FT DOMAIN 109 187
 FT DOMAIN 215 292
 FT DOMAIN 361 618
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 FT DISULFID 333 479

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 SQ SEQUENCE 618 AA; 70268 MW; B89F719AAFD601E0 CRC64;

Query Match 47.1%; Score 90; DB 1; Length 618;
 Best Local Similarity 39.5%; Pred. No. 4.5e-08;
 Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 2 NAFLLXLRGSLRXCKXCQSPFXAFXIFKDXARTLFWISY 44
 DB 46 SGFLIEIRKGNLEBCEVEBCSTEBEALEALFSDTDVFWAKY 88

RESULT 15
 ID PRTC_BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV) (Fragment).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP MEDLINE=6091100;
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RN [2]
 RP MEDLINE=6896876;
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RT "Amino acid sequence of the light chain of bovine protein C";
 RT J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RT "beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RT Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RT "Amino acid sequence of the heavy chain of bovine protein C";
 RT J. Biol. Chem. 257:12180-12190(1982).
 RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Emon N.L., Debaule L.E., Emon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 RT domainless protein C";
 RT J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Emon N.L., Laue T.M., Emon C.T.;
 RT "Structural changes required for activation of protein C are induced
 RT by Ca2+ binding to a high affinity site that does not contain gamma-
 RT carboxyglutamic acid";
 RT J. Biol. Chem. 258:5554-5560(1983).
 RL

- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.

- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPETIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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DR PIR; A00928; KXBO.

DR HSSP; P04070; 1PCU.

DR MEROPS; S01.218; -.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00594; gla; 1.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; TYPD_SPC; 1.

DR PROSITE; PS00010; Asx_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF CA; 1.

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Glycoprotein; Serine protease;

KW Gamma-carboxylglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.

FT NON_TER 1 1

FT SIGNAL <1 29

FT PROPEP 30 39

FT CHAIN 40 194

FT CHAIN 197 456

FT PEPTIDE 197 210

FT DOMAIN 94 129

FT DOMAIN 133 173

FT DOMAIN 211 456

FT MOD_RES 45 45

FT MOD_RES 46 46

FT MOD_RES 53 53

FT MOD_RES 55 55

FT MOD_RES 58 58

FT MOD_RES 59 59

FT MOD_RES 62 62

FT MOD_RES 64 64

FT MOD_RES 65 65

PROTEIN C LIGHT CHAIN.

PROTEIN C HEAVY CHAIN.

ACTIVATION PEPTIDE.

EGF-LIKE 1.

EGF-LIKE 2.

SERINE PROTEASE.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.

FT	MOD_RES	68	68	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	74	74	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	110	110	HYDROXYLATION.
FT	ACT_SITE	252	252	CHARGE RELAY SYSTEM.
FT	ACT_SITE	298	298	CHARGE RELAY SYSTEM.
FT	ACT_SITE	397	397	CHARGE RELAY SYSTEM.
FT	DISULFID	56	61	BY SIMILARITY.
FT	DISULFID	89	108	BY SIMILARITY.
FT	DISULFID	98	103	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	119	128	BY SIMILARITY.
FT	DISULFID	137	148	BY SIMILARITY.
FT	DISULFID	144	157	BY SIMILARITY.
FT	DISULFID	159	172	BY SIMILARITY.
FT	DISULFID	180	318	INTERCHAIN.
FT	DISULFID	227	253	
FT	DISULFID	368	382	
FT	DISULFID	393	421	
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	289	289	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	366	366	N-LINKED (GLCNAC. . .).
FT	VARIANT	82	82	F -> K.
FT	CONFLICT	455	456	VP -> PV (IN REF. 4).
FT	CONFLICT	455	456	CAA6833F894C209 CRC64;
FT	SEQUENCE	456 AA;	51407 MW;	

Query Match 46.1%; Score 88; DB 1; Length 456;

Best Local Similarity 40.9%; Pred. No. 7; Se-08;

Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLLXLRREGSLRXCKXKXCSFXXAFXIFPDAXRTKLFMTSY 44

DB 40 ANSFLEBLRPNVNERCSEVECFEFARREIFONTEDTMAFMSFY 83

Search completed: March 19, 2003, 14:52:50

Job time : 6.625 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFPLXLRGSLXRXCKXK.....XXAFYFKDAXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	81.7	701	4 Q96PQ8	Q96PQ8 homo sapien
2	111	58.1	446	11 Q61109	Q61109 mus musculu
3	97	50.8	460	11 Q91WN8	Q91WN8 mus musculu
4	94	49.2	100	4 Q15253	Q15253 homo sapien
5	91	47.6	460	11 Q99PC6	Q99PC6 mus musculu
6	90	47.1	482	11 Q63207	Q63207 ratus norv
7	88	46.1	456	6 Q9TTR0	Q9TTR0 canis fami
8	88	46.1	469	6 Q9GMD9	Q9GMD9 ornithorhyn
9	88	46.1	481	11 Q54740	Q54740 mus musculu
10	88	46.1	481	11 Q91J32	Q91J32 mus musculu
11	88	46.1	481	11 Q88947	Q88947 mus musculu
12	78	40.8	49	6 Q95ME8	Q95ME8 bos taurus
13	77	40.3	456	4 Q14316	Q14316 homo sapien
14	77	40.3	461	6 Q95ND7	Q95ND7 pan troglod
15	77	40.3	461	6 Q95ND6	Q95ND6 pan troglod
16	73	38.2	179	4 Q8TMS3	Q8TMS3 homo sapien

17	73	38.2	198	11 Q8R182	Q8R182 mus musculu
18	72	37.7	608	13 Q9PTW7	Q9PTW7 struthio ca
19	71	37.2	138	6 Q28994	Q28994 sus scrofa
20	69	36.1	607	13 Q91001	Q91001 gallus gall
21	67	35.1	433	13 Q90YK1	Q90YK1 brachydanio
22	64	33.5	648	6 Q29094	Q29094 sus scrofa
23	62	32.5	98	13 P82807	P82807 notechis sc
24	61	31.9	399	11 Q9COW3	Q9COW3 mus musculu
25	59	30.9	650	4 Q9NSD0	Q9NSD0 homo sapien
26	59	30.9	650	4 Q16519	Q16519 homo sapien
27	55.5	29.1	431	10 Q94EY5	Q94EY5 arabidopsis
28	55.5	29.1	492	10 Q9SMJ7	Q9SMJ7 cicer arlet
29	55.5	29.1	543	10 Q9MB23	Q9MB23 arabidopsis
30	55.5	29.1	576	10 Q9CV94	Q9CV94 arabidopsis
31	55.5	29.1	589	10 Q9LMS2	Q9LMS2 arabidopsis
32	55	28.8	25	11 Q9QVH6	Q9QVH6 ratus sp.
33	54.5	28.5	196	10 Q04284	Q04284 selaginella
34	54.5	28.5	542	5 Q8T613	Q8T613 halocynthia
35	53.5	28.0	459	10 Q9SE22	Q9SE22 oryza sativ
36	52.5	27.5	506	10 Q9SPF0	Q9SPF0 oryza sativ
37	52.5	27.5	506	10 Q9SE23	Q9SE23 oryza sativ
38	52.5	27.5	567	10 Q8W4J2	Q8W4J2 arabidopsis
39	51.5	27.0	510	10 Q9MB22	Q9MB22 arabidopsis
40	51.5	27.0	619	10 Q9LV37	Q9LV37 arabidopsis
41	50	26.2	673	11 Q61592	Q61592 mus musculu
42	50	26.2	674	11 Q99K57	Q99K57 mus musculu
43	49.5	25.9	588	10 Q91M33	Q91M33 arabidopsis
44	49.5	25.9	603	10 Q91PC7	Q91PC7 arabidopsis
45	49.5	25.9	606	10 Q9SUG9	Q9SUG9 arabidopsis

ALIGNMENTS

RESULT 1
Q96PQ8 PRELIMINARY; PRT; 701 AA.
ID Q96PQ8
AC Q96PQ8; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001861; EGF-Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; Vtck_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.

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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match
Best Local Similarity 81.7%; Score 156; DB 4; Length 701;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXXAFXIFKDXARTKLFWISY 44
DB 61 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 2
ID 061109 PRELIMINARY; PRT; 446 AA.
AC 061109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=66276538; PubMed=8701412;
RA Idusogile E., Kosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY

DR EMBL; U04795; AAC52570.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_spc; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 58.1%; Score 111; DB 11; Length 446;
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Best Local Similarity 54.5%; Pred. No. 3.3e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXXAFXIFKDXARTKLFWISY 44
DB 42 ANSFLLEMRPGSLRECKNECCSFEEAREIFKSPERTKOFWIVY 85

RESULT 3
ID 091WN8 PRELIMINARY; PRT; 460 AA.
AC 091WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (Sep--2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.5e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXXAFXIFKDXARTKLFWISY 44
DB 42 ANSFLLEMRPGSLRECKNEICDFEEAOEIFONVEDTLAFWIKY 85

RESULT 4
ID 015253 PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA Macgillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;
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RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PFI.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Signal.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; F0D85D0174E1F6FE CRC64;

Query Match 49.2%; Score 94; DB 4; Length 100;
Best Local Similarity 38.6%; Pred. No. 1.1e-09;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLXXLRGSLRXKCKXQGFXXAFIFDAXRTKLFWISY 44
DB 44 ANTFLEVRKGNLERECVETCSYEAFELBSSTATDVMARY 87

RESULT 5
O99PC6 PRELIMINARY; PRT; 460 AA.
AC O99PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF318182; AKK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00020; TRYP_SPC; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00013; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25ED3ED16 CRC64;

Query Match 47.6%; Score 91; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.9e-08;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLXXLRGSLRXKCKXQGFXXAFIFDAXRTKLFWISY 44
DB 42 ANSFLEMRPGSLRECMERICDLEERQETFQVEDTLAFWIKY 85

RESULT 6
O63207 PRELIMINARY; PRT; 482 AA.
AC O63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RC MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase."
RL Thromb. Res. 80:63-73(1995).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1XXA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 47.1%; Score 90; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 3.1e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
```



```
GN F10 OR FA10.
OS Mus musculus (Mouse).
OC Plasmid pBluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=9645493; PubMed=9783672;
RA Heilmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
CC EMBL: A222677; CAA10933.1; -.
DR HSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00017; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00020; TRY_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53966 MW; CF702DSEFD97AE CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRBGLSRXCKXXQCSFXXAFIFKDAKTKLFWISY 44
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DB 41 ANSFEEFKGNLRECMETICSYEEVREIFEDDEKTEKWTXY 84

RESULT 10
O99L32 PRELIMINARY; PRT; 481 AA.
AC O99L32;
DT 01-UN-2001 (TREMBlrel. 17, Created)
DT 01-UN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-UN-2002 (TREMBlrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
CC EMBL: BC003877; AAH03877.1; -.
DR HSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRBGLSRXCKXXQCSFXXAFIFKDAKTKLFWISY 44
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 41 ANSFEEFKGNLRECMETICSYEEVREIFEDDEKTEKWTXY 84

RESULT 11
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=129S;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DB EMBL; AF087644; AAC36345.1; -.
DB EMBL; AF211347; AAF22980.1; -.
DB HSSP; P00742; 1XKA.
DB MEROPS; S01.216; -.
DB MGD; MGI:103107; P10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT CHAIN 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EEF9D271E CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLKRCXKQCFXKAPXIFKDAKRTKLFWISY 44
DB 41 ANSFFERKKNLRBCEMEICSYEVRVEITFDEDEKTEVTKY 84

RESULT 12
Q9SMER PRELIMINARY; PRT; 49 AA.
AC Q9SMER;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amara E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF34598; AAK7556.1; -.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

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FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 40.8%; Score 78; DB 6; Length 49;
Best Local Similarity 41.2%; Pred. No. 5.3e-07;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSILRXCKXKQCFXKAPXIFKDAKRTKLFWISY 44
DB 15 GNLERCKEKCKSFEEAREVENTETTERFQY 48

RESULT 13
Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=8327116; PubMed=3416069;
RA Riltma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Brier E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988)
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DB EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLA_BLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

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Query Match          40.3%; Score 77; DB 4; Length 456;
Best Local Similarity 40.0%; Pred. No. 8.2e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRCKXKQCSFYXAFIFPDARTKLFWISY 44
DB 52 QGNLERECMEKCSFEAREVFENTERTEFWKQY 86

RESULT 14
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees."
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
DR HydroLase; Serine protease.
SQ SEQUENCE 461 AA, 51764 MW, 30C2F857C0F77F45 CRC64;

Query Match          40.3%; Score 77; DB 6; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.3e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRCKXKQCSFYXAFIFPDARTKLFWISY 44
DB 57 QGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 15
Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
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DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees."
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; JOINED.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
DR HydroLase; Serine protease.
SQ SEQUENCE 461 AA, 51695 MW, 8F5A69A525DF65B5 CRC64;

Query Match          40.3%; Score 77; DB 6; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.3e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRCKXKQCSFYXAFIFPDARTKLFWISY 44
DB 57 QGNLERECMEKCSFEAREVFENTERTEFWKQY 91
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Job time : 47.3125 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLU28PHE

Perfect score: 191

Sequence: 1 ANAFIXLREGSLRXRCXXX.....XXAFXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.4	44	3	US-08-955-636-28 Sequence 28, Appl
2	162	84.8	44	3	US-08-955-636-26 Sequence 26, Appl
3	159	83.2	44	3	US-08-955-636-27 Sequence 27, Appl
4	156	81.7	44	3	US-08-955-636-3 Sequence 3, Appl
5	156	81.7	406	1	US-08-293-778-24 Sequence 24, Appl
6	156	81.7	406	1	US-08-295-411-5 Sequence 5, Appl
7	156	81.7	406	2	US-08-955-471-5 Sequence 5, Appl
8	156	81.7	406	5	PCT-US92-10242-5 Sequence 5, Appl
9	156	81.7	444	1	US-08-475-845-2 Sequence 2, Appl
10	156	81.7	444	2	US-08-327-690-2 Sequence 2, Appl
11	156	81.7	444	2	US-08-660-289-2 Sequence 2, Appl
12	156	81.7	444	2	US-08-537-807-2 Sequence 2, Appl
13	156	81.7	444	2	US-08-871-003-2 Sequence 2, Appl
14	156	81.7	444	3	US-08-464-233-2 Sequence 2, Appl
15	156	81.7	444	4	US-09-189-607-2 Sequence 2, Appl
16	156	81.7	444	4	US-09-378-907-2 Sequence 2, Appl
17	156	81.7	444	5	PCT-US94-05779-2 Sequence 2, Appl
18	156	81.7	466	1	US-07-882-2024-4 Sequence 4, Appl
19	156	81.7	466	1	US-08-321-777-4 Sequence 4, Appl
20	156	81.7	466	1	US-08-321-777-4 Sequence 4, Appl
21	156	81.7	466	4	US-09-009-217-14 Sequence 14, Appl
22	156	81.7	466	4	US-09-009-656-14 Sequence 4, Appl
23	156	81.7	466	5	PCT-US93-04493-4 Sequence 4, Appl
24	155	81.2	44	3	US-08-955-636-30 Sequence 30, Appl
25	150	78.5	44	3	US-08-955-636-29 Sequence 4, Appl
26	141	73.8	41	1	US-08-229-280-4 Sequence 4, Appl
27	122	63.9	44	3	US-08-955-636-4 Sequence 4, Appl

28	105	55.0	139	1	US-08-330-978-2 Sequence 2, Appl
29	105	55.0	139	1	US-08-474-042-2 Sequence 2, Appl
30	105	55.0	139	1	US-08-484-558-2 Sequence 2, Appl
31	105	55.0	139	1	US-08-774-592-2 Sequence 2, Appl
32	105	55.0	437	1	US-08-487-037-2 Sequence 2, Appl
33	105	55.0	437	1	US-08-487-037-3 Sequence 3, Appl
34	105	55.0	488	1	US-08-487-037-1 Sequence 1, Appl
35	97	50.8	44	3	US-08-955-636-35 Sequence 35, Appl
36	96	50.3	44	3	US-08-955-636-18 Sequence 18, Appl
37	96	50.3	448	1	US-08-295-411-3 Sequence 3, Appl
38	96	50.3	448	2	US-08-955-471-3 Sequence 3, Appl
39	96	50.3	448	5	PCT-US92-10068-1 Sequence 1, Appl
40	96	50.3	448	5	PCT-US92-10242-3 Sequence 3, Appl
41	96	50.3	487	1	US-08-469-486-53 Sequence 53, Appl
42	96	50.3	487	2	US-08-469-658-53 Sequence 2, Appl
43	96	50.3	492	1	US-08-469-486-2 Sequence 2, Appl
44	96	50.3	492	2	US-08-469-658-2 Sequence 2, Appl
45	95	49.7	44	3	US-08-955-636-25 Sequence 25, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      86.4%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 36-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFIXLREGSLRXRCXXXCFXAFXIFKDXRTKLFWISY 44
DB 1 ANAFIXLREGSLRXRCXXXCFXAFXIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match
Best Local Similarity 97.7%; Pred. No. 9, 6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 3
US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelisestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match
Best Local Similarity 95.5%; Pred. No. 3, 1e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 4
US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelisestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match
Best Local Similarity 95.5%; Pred. No. 1e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 5
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolsen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiber, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agri's, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match
Best Local Similarity 81.7%; Score 156; DB 1; Length 406;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLLXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 6
US-08-295-411-5


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/
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10242
/ FILING DATE: 19921118
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Filting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCRO472P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..152
/ OTHER INFORMATION: /note= "Factor VII Light Chain"
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 153..406
/ OTHER INFORMATION: /note= "Factor VII Heavy Chain"
/
/ PCT-US92-10242-5

Query Match 81.7%; Score 156; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLXRXCKXXQCSFXXAFXIKDAXRTKLFWISY 44
Db 1 ANAFLBELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9
US-08-475-845-2
/ Sequence 2, Application US/08475845
/ Patent No. 5788965
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/08/475,845
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-475-845-2
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Query Match 81.7%; Score 156; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1,2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLXXLRGSLXRXCKXXQCSFXXAFXIKDAXRTKLFWISY 44
Db 39 ANAFLBELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82
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RESULT 10
US-08-327-690-2
/ Sequence 2, Application US/08327690
/ Patent No. 5817788
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
```

FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLRXCKXQCSFYXAFIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAXRTKLFWISY 82

RESULT 11
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLRXCKXQCSFYXAFIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAXRTKLFWISY 82

RESULT 12
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLRXCKXQCSFYXAFIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAXRTKLFWISY 82

RESULT 13
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.

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; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Raemussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-003-2

Query Match      81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLKRXCKXQCSFXAXFIKDXARTKLFWISY 44
Db 39 ANAFLELRPGSLRECKECCSFEEARELTKDARITLFWISY 82

RESULT 14
US-08-464-233-2
; Sequence 2, Application US/08464233
; Patent No. 6039944
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-233-2

Query Match      81.7%; Score 156; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLKRXCKXQCSFXAXFIKDXARTKLFWISY 44
Db 39 ANAFLELRPGSLRECKECCSFEEARELTKDARITLFWISY 82

RESULT 15
US-09-189-607-2
; Sequence 2, Application US/09189607
; Patent No. 618789
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,607
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,289
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/662,920
 ; FILING DATE: 28-FEB-1991
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-8-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-467-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 444 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-189-607-2

Query Match 81.7%; Score 156; DB 4; Length 444;
 Best Local Similarity 72.7%; Pred. No. 1,2e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXXQCSFXXAFXIFKDAARTKLFWISY 44
 Db 39 ANAFLEELRPGSLRECKEKEQCSFEARARIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:15
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFILXLRGSLRXKXCKX.....XXAFYIFDAXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues
Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	406	US-10-109-498-1	Sequence 1, Appli
2	94	49.2	419	US-10-182-263-6	Sequence 6, Appli
3	92	48.2	419	US-10-182-263-3	Sequence 3, Appli
4	92	48.2	419	US-10-182-263-4	Sequence 4, Appli
5	92	48.2	419	US-10-182-263-5	Sequence 5, Appli
6	81	42.4	419	US-10-182-263-1	Sequence 1, Appli
7	81	42.4	419	US-09-978-917A-4	Sequence 4, Appli
8	81	42.4	461	US-10-182-263-2	Sequence 2, Appli
9	81	42.4	461	US-09-978-917A-2	Sequence 2, Appli
10	77	40.3	415	US-09-118-748-2	Sequence 2, Appli
11	77	40.3	461	US-10-132-829-5	Sequence 5, Appli
12	77	40.3	461	US-09-884-901-3	Sequence 3, Appli
13	66.5	34.8	96	US-09-759-1308-313	Sequence 313, App
14	66.5	34.8	209	US-09-759-1308-312	Sequence 312, App
15	66.5	34.8	226	US-09-759-1308-310	Sequence 310, App
16	51.5	27.0	95	US-09-759-1308-356	Sequence 356, App
17	51.5	27.0	208	US-09-759-1308-355	Sequence 355, App
18	51.5	27.0	225	US-09-759-1308-353	Sequence 353, App
19	45.5	23.8	729	US-10-145-396-11	Sequence 11, Appli

20	44.5	23.3	347	10	US-09-780-053-4	Sequence 4, Appli
21	44.5	23.3	730	9	US-10-145-396-12	Sequence 12, Appli
22	44.5	23.3	730	10	US-09-780-053-2	Sequence 2, Appli
23	43	22.5	447	10	US-09-815-242-13490	Sequence 13490, A
24	43	22.5	447	10	US-09-815-242-13612	Sequence 13612, A
25	43	22.5	447	10	US-09-735-564-2	Sequence 2, Appli
26	41	21.5	447	10	US-09-811-284-194	Sequence 194, App
27	40	20.9	240	9	US-09-782-504-4	Sequence 4, Appli
28	40	20.9	273	9	US-09-764-868-968	Sequence 968, App
29	39	20.4	115	9	US-09-883-152-21	Sequence 21, Appli
30	39	20.4	115	9	US-09-986-480-132	Sequence 132, App
31	39	20.4	130	9	US-09-986-480-345	Sequence 345, App
32	39	20.4	254	9	US-10-104-019-21	Sequence 21, Appli
33	39	20.4	873	9	US-10-200-154-2	Sequence 2, Appli
34	39	20.4	873	10	US-09-954-043-2	Sequence 2, Appli
35	38.5	20.2	111	10	US-09-899-896-7	Sequence 7, Appli
36	38	19.9	47	10	US-09-733-254-109	Sequence 109, App
37	38	19.9	47	10	US-09-904-615-109	Sequence 109, App
38	38	19.9	176	9	US-10-078-770-106	Sequence 106, App
39	38	19.9	179	9	US-09-738-626-6259	Sequence 6259, App
40	38	19.9	333	9	US-09-738-626-5683	Sequence 5683, App
41	38	19.9	400	9	US-10-078-770-114	Sequence 114, App
42	38	19.9	467	10	US-09-912-020-381	Sequence 381, App
43	38	19.9	608	10	US-09-908-664-5	Sequence 5, Appli
44	38	19.9	1266	9	US-09-931-969A-2	Sequence 2, Appli
45	38	19.9	1266	9	US-10-079-699-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286-200-US
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match 81.7%; Score 156; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 5.2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFILXLRGSLRXKXCKXCSFXAFYIFDAXRTKLFWISY 44
DB 1 ANAFILXLRGSLRXKXCKXCSFXAFYIFDAXRTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

```

; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          49.2%; Score 94; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 7.1e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXAXFIFKDAKRTKLFW 41
Db 1 ANSFLELRHSSLRRCIEICDFEAKKEIFQVDDTLAFW 41

RESULT 7
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1

; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - Protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXAXFIFKDAKRTKLFW 41
Db 1 ANSFLELRHSSLRRCIEICDFEAKKEIFQVDDTLAFW 41

RESULT 8
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXAXFIFKDAKRTKLFW 41
Db 43 ANSFLELRHSSLRRCIEICDFEAKKEIFQVDDTLAFW 83

RESULT 9

US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:

; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - Protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXAXFIFKDAKRTKLFW 41
Db 43 ANSFLELRHSSLRRCIEICDFEAKKEIFQVDDTLAFW 83

RESULT 10
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Actively
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match
Best Local Similarity 40.3%; Score 77; DB 10; Length 415;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 10 EGSLLRXCKXQCSFXAXFIFKDAKRTKLFWISY 44
Db 11 QGNLRECEWEKCSFEAREVEFENTERTEFPWKQY 45

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:

; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-PAL170

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/ CURRENT APPLICATION NUMBER: US/10/132.829
/ CURRENT FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: 60/286,314
/ PRIOR FILING DATE: 2001-04-25
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-132-829-5

Query Match          40.3%; Score 77; DB 9; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.8e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY      10 EGSIXRXXKXXQCSFXAXFXIFKDXRXTKLFWISY 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      57 QGNLRECMEEKCSFEERAREVFENTERTTERFWKQY 91

RESULT 12
/ US-09-884-901-3
/ Sequence 3, Application US/09884901
/ Patent No. US20020076798A1
/ GENERAL INFORMATION:
/ APPLICANT: Miao, Carol
/ APPLICANT: Kay, Mark
/ TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
/ FILE REFERENCE: UOFW-1-17396
/ CURRENT APPLICATION NUMBER: US/09/884,901
/ CURRENT FILING DATE: 2001-06-18,902
/ PRIOR APPLICATION NUMBER: US 60/212,902
/ PRIOR FILING DATE: 2000-06-20
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapien
/ US-09-884-901-3

Query Match          40.3%; Score 77; DB 10; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.8e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY      10 EGSIXRXXKXXQCSFXAXFXIFKDXRXTKLFWISY 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      57 QGNLRECMEEKCSFEERAREVFENTERTTERFWKQY 91

RESULT 13
/ US-09-759-130B-313
/ Sequence 313, Application US/09759130B
/ Publication No. US20030022279A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Fraser, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirst, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodearl, Andrew
/ APPLICANT: Holzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ FILE REFERENCE: MPI00-535OMNIM
/ CURRENT APPLICATION NUMBER: US/09/759,130B
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/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 313
/ LENGTH: 96
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-759-130B-313

Query Match          34.8%; Score 66.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 0.00013;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLXRXKXXQCSFXAXFXIFKDXRXTKLFWISY 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      36 NRPDLLEFTPGNLERECNEELCNVEAREIFVDEDKTIAFWQEX 79

RESULT 14
/ US-09-759-130B-312
/ Sequence 312, Application US/09759130B
/ Publication No. US20030022279A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Fraser, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirst, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodearl, Andrew
/ APPLICANT: Holzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ FILE REFERENCE: MPI00-535OMNIM
/ CURRENT APPLICATION NUMBER: US/09/759,130B
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 313
/ LENGTH: 96
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-759-130B-312
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match      34.8%; Score 66.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLRXCKXQCSFXXAFKPKDAXRTKLFWISY 44
Db      36 NRPDLFLFTPGNLRRCNELCNVEEARLIFVDEDKTIAFWQRY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodenartl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

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Best Local Similarity 36.4%; Pred. No. 0.00032;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLRXCKXQCSFXXAFKPKDAXRTKLFWISY 44
Db      53 NRPDLFLFTPGNLRRCNELCNVEEARLIFVDEDKTIAFWQRY 96
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Search completed: March 20, 2003, 13:30:12
Job time : 9.375 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLLXNGSLXRCRX.....XXAEXIFRNXXRTRFWVSV 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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23: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	81.6	44	20	AAV18306
2	155	81.6	44	22	AAAB36396
3	125	65.8	44	20	AAV18311
4	124	65.3	44	20	AAV18310
5	122	64.2	44	20	AAV18302
6	122	64.2	44	20	AAV18305
7	122	64.2	44	22	AAAB36395
8	122	64.2	401	22	AAAB4870
9	122	64.2	401	22	AAAB4871
10	122	64.2	406	14	AAAB35764

11	122	64.2	406	18	AAW14509	Modified blood coa
12	122	64.2	406	18	AAW14510	Modified blood coa
13	122	64.2	406	22	AAU77745	Human factor VIIa
14	122	64.2	406	22	AAW52171	Human FVII SEQ ID
15	122	64.2	406	22	AAW52172	Mammalian expressed
16	122	64.2	406	22	AAW52181	Human FVII mutant
17	122	64.2	406	22	AAW52182	Human FVII mutant
18	122	64.2	406	22	AAW52183	Human FVII mutant
19	122	64.2	406	22	AAW52184	Human FVII mutant
20	122	64.2	406	22	AAW52185	Human FVII mutant
21	122	64.2	406	22	AAW52186	Human FVII mutant
22	122	64.2	406	22	AAW52187	Human FVII mutant
23	122	64.2	406	22	AAW52188	Human FVII mutant
24	122	64.2	406	22	AAW52189	Human FVII mutant
25	122	64.2	406	22	AAW52190	Human FVII mutant
26	122	64.2	406	22	AAW52191	Human FVII mutant
27	122	64.2	406	22	AAW52192	Human FVII mutant
28	122	64.2	406	22	AAW52193	Human FVII mutant
29	122	64.2	406	22	AAW52194	Human FVII mutant
30	122	64.2	406	22	AAW52195	Human FVII mutant
31	122	64.2	406	22	AAW52196	Human FVII mutant
32	122	64.2	406	22	AAW52197	Human FVII mutant
33	122	64.2	406	22	AAW52198	Human FVII mutant
34	122	64.2	406	22	AAW52199	Human FVII mutant
35	122	64.2	406	22	AAW52200	Human FVII mutant
36	122	64.2	406	22	AAW52201	Human FVII mutant
37	122	64.2	406	22	AAW52202	Human FVII mutant
38	122	64.2	406	22	AAW52203	Human FVII mutant
39	122	64.2	406	22	AAW52204	Human FVII mutant
40	122	64.2	406	22	AAW52205	Human FVII mutant
41	122	64.2	406	22	AAW52206	Human FVII mutant
42	122	64.2	406	22	AAW52207	Human FVII mutant
43	122	64.2	406	22	AAW52208	Human FVII mutant
44	122	64.2	406	22	AAW52209	Human FVII mutant
45	122	64.2	406	22	AAW52210	Human FVII mutant

ALIGNMENTS

RESULT 1	AAV18306	standard; peptide; 44 AA.
ID	AAV18306	
XX	AAV18306;	
AC	AAV18306;	
DT	17-ANG-1999	(first entry)
XX		
DE	Bovine factor VII GLA domain.	
XX		
KW	GLA domain; vitamin K-dependent protein; clotting disorder;	
KM	therapy.	
XX		
OS	Bos taurus.	
XX		
FH	Key	location/Qualifiers
FT	Misc-difference 1..44	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT		
XX		
PN	WO9920767-A1.	
XX		
PD	29-APR-1999.	
XX		
XX	20-OCT-1998;	98WO-US22152.
PF		
XX		
PR	23-OCT-1997;	97US-0955636.
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
XX	Neisestuen GL;	
PI		
XX		
DR	WPI; 1999-288309/24.	

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 81.6%; Score 155; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.8e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1 ANGFLXLLRNGSLXRCXRLCSFXXAEXIFRNXXRTQFWVS 44
1 ANGFLXLLRPGSLXRCXRLCSFXXAHXIFRNXXRTQFWVS 44
Db
XX
RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
XX
AC AAB36396;
XX
DT 27-FEB-2001 (first entry)
XX
DE Bovine factor VII gamma-carboxyglutamic acid domain SRQ ID NO:4.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
OS Bos taurus.
XX
XX WO200066753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Neiseetuen GL;
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity -
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;
XX
Query Match 81.6%; Score 155; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.8e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1 ANGFLXLLRNGSLXRCXRLCSFXXAEXIFRNXXRTQFWVS 44
1 ANGFLXLLRPGSLXRCXRLCSFXXAHXIFRNXXRTQFWVS 44
Db
XX
RESULT 3
AA18311
ID AA18311 standard; peptide; 44 AA.
XX
AC AA18311;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44 "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Neiseetuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 65.8%; Score 125; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.5e-13;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
 DB 1 ANAFLLXXLRGSLRXCRXXQCSPFXAEXIFKDXRTKLFWISY 44

RESULT 4
 ID AAY18310 standard; peptide; 44 AA.
 XX AAY18310;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN MO920767-A1.

PD 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

XX 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

XX Nelsestuen GL;

XX WPI, 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders

XX PS Disclosure; Page 80; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

XX SQ Sequence 44 AA;

Query Match 65.3%; Score 124; DB 20; Length 44;

Best Local Similarity 75.0%; Pred. No. 6.5e-13;

Matches 33; Conservativity 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
 DB 1 ANAFLLXXLRGSLRXCRXXQCSPFXAEXIFKDXRTKLFWISY 44

RESULT 5
 ID AAY18302 standard; peptide; 44 AA.

XX AAY18302;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN MO920767-A1.

PD 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

XX 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

XX Nelsestuen GL;

XX WPI, 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders

XX Claim 11; Page 81; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

XX SQ Sequence 44 AA;

Query Match 64.2%; Score 122; DB 20; Length 44;

Best Local Similarity 75.0%; Pred. No. 1.4e-12;

Matches 33; Conservativity 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAEXIFRNXXRTROPWVS 44
 DB 1 ANAFLLXXLRGSLRXCRXXQCSPFXAEXIFKDXRTKLFWISY 44

RESULT 6
 ID AAY18305 standard; peptide; 44 AA.
 XX AAY18305;

DT 17-AUG-1999 (first entry)

DE Human factor VII GLA domain.

KM GLA domain; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN MO920767-A1.

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XX 29-APR-1999.
PD 20-OCT-1998; 98WO-US22152.
XX 23-OCT-1997; 97US-0955636.
XX (MINU ) UNIV MINNESOTA.
PA (MINU ) UNIV MINNESOTA.
PI Neiseetuen GL;
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
CC
XX Sequence 44 AA;
SQ
Query Match 64.2%; Score 122; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44
Db 1 ANAFLXXLRPGSLKRXCRXXLCSPFXAEXIFRNXXRTQFWIS 44
RESULT 7
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX AAB36395;
AC
XX
XX 27-FEB-2001 (first entry)
DT
XX
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
DE
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KM factor X; prothrombin; enhanced membrane binding affinity;
KM clot formation; thrombolytic; haemostatic; bleeding disorder;
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM liver disease.
XX
XX Homo sapiens.
OS
XX
XX WO20006753-A2.
XX
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-US11416.
PF
XX
XX 29-APR-1999; 99US-0302239.
PR
XX
XX (MINU ) UNIV MINNESOTA.
PA
XX
XX Neiseetuen GL;
PI
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified

```

```

PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX Sequence 44 AA;
SQ
Query Match 64.2%; Score 122; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44
Db 1 ANAFLXXLRPGSLKRXCRXXLCSPFXAEXIFRNXXRTQFWIS 44
RESULT 8
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX AAB84870;
AC
XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Mutant blood coagulant factor VII (FVII-31).
DE
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; mutlein.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Ala substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
XX
XX 24-AUG-1999; 99JP-0237610.
PF
XX
XX 24-AUG-1999; 99JP-0237610.
PR
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA
XX
XX WPI; 2001-310677/33.
DR N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.

```

```

XX Sequence      401 AA;
SO Query Match          64.2%; Score 122; DB 22; Length 401;
   Best Local Similarity 52.3%; Pred. No. 1.2e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 1 ANGFLLXLRNGSLRXCRXXLCSPFXXAEXIFPNXXRTROFWMVSY 44
    |||||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 ANAFLEELRPGSLERECKEEOCSFEAREEIFDASRTKLFWISY 44
                                     .
RESULT 9
ID AAB84871 standard; Protein; 401 AA.
XX AAB84871;
AC
XX AAB84871;
AC
XX 31-JUL-2001 (first entry)
DT
DE Mutant blood coagulant factor VII (FVII-39).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; muteln.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317 /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT FT Ser-Ileu substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
PF 24-AUG-1999; 99JP-0237610.
XX
PR 24-AUG-1999; 99JP-0237610.
XX
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI: 2001-310677/33.
DR N-PSDB: AAH19464.
XX
PT Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
PS Claim 16; Page 23-24; 29pp; Japanese.
XX
CC The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
SQ Sequence 401 AA;
Query Match          64.2%; Score 122; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.2e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 1 ANGFLLXLRNGSLRXCRXXLCSPFXXAEXIFPNXXRTROFWMVSY 44
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Db 1 ANAFLEELRPGSLERECKEEOCSFEAREEIFDASRTKLFWISY 44

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XX	AAR35764;
AC	
XX	24-SEP-1993 (first entry)
DT	
XX	Factor VII (VII).
DE	
XX	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW	Factor VII; CT; Chymotrypsinogen; SP; serine protease; binding;
KM	exosite; catalytic activity.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	/note= "Factor VII light chain"
FT	1..152
FT	/note= "Factor VII heavy chain"
FT	153..406
FT	/note= "Factor VII heavy chain"
FT	374..388
FT	/note= "exosite 1"
FT	290..310
FT	/note= "exosite 2"
FT	290..310
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	374..388
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	289..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	290..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	245..266
FT	/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
FN	WO9309804-A.
XX	
PD	27-MAY-1993.
XX	
PF	18-NOV-1992; 92WO-US10242.
XX	
PR	18-NOV-1991; 91US-0793989.
XX	
PA	(SCRI) SCRIPPS RES INST.
XX	
PI	Griffin JH, Meesters RM;
DR	WP1; 1993-182244/22.
XX	
PT	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
PS	Disclosure; Page 133-135; 14pp; English.
XX	
CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm.
CC	NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
SO	Sequence 406 AA;
Oy	Query Match 64.2%; Score 122; DB 14; Length 406; Best Local Similarity 52.3%; Pred. No. 1,2e-11; Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
bh	1 ANGFLLXLRNGSLKRXCRXXLCSPFXAEXIRNXXRTQFPWVS 44 1 ANAFLLELRPGSLERKECKEQCFEAEATRFKDARTYLFWISY 44

KW	Factor VIIa; human; shock heat treatment; protein stability;
KW	protein manufacture; protein conformation; mutant; mutain.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Active-site
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Active-site
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Active-site
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Misc-difference
FT	344
FT	/label= Gly, Met, Thr
FT	/note= "Preferably Ala. Wild type Ser"
XX	
PN	WO200177141-A1.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-DK00234.
XX	
PR	06-APR-2000; 2000DK-0000573.
PR	17-APR-2000; 2000US-197650P.
XX	
PA	(NOVO) NOVO NORDISK AS.
XX	
PI	Matthiesen F;
XX	
DR	WPI; 2001-657162/75.
XX	
PT	Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX	
PT	involves a shock heat treatment -
XX	
BS	Disclosure; Page -; 22pp; English.
XX	
CC	The invention describes a method of stabilising a polypeptide involving
CC	shock heat treatment of the polypeptide. The method is useful in a
CC	pharmaceutical composition, in the industrial or large scale method of
CC	manufacturing a polypeptide, also as a unit operation during preparation,
CC	purification, recovery and/or formulation of polypeptides. The shock heat
CC	treatment improves the protein stability without substantial loss of
CC	biological activity. The method can be applied to change polypeptide
CC	conformation in a very fast and non-invasive manner. The polypeptide
CC	formed is stable. The method is also useful for decreasing the
CC	association of the polypeptide. This sequence represents a modified
CC	human factor VIIa protein, mutated at the catalytic site, described
CC	in the invention.
CC	Note: This sequence does not appear in the specification but has
CC	been obtained using information given in the invention.
XX	
SQ	Sequence 406 AA;
XX	
Query Match	64.2%; Score 122; DB 22; Length 406;
Best Local Similarity	52.3%; Pred. No. 1, 2e-11;
Matches 23; Conservative	5; Mismatches 16; Indels 0; Gaps 0
OY	1 ANGELXXLRNGSLXKRCXKXLCSEFXAEXIFRNXXTRQFWSY 44
DB	1 ANAFLEELRPGSLERCKEEOCSFEARELIFDAERTKULFWISY 44
XX	
RESULT 14	
AAM52171	
ID	AAM52171 standard; Protein; 406 AA.
XX	
AC	AAM52171;
XX	
DT	07-FEB-2002 (first entry)
XX	
DE	Human FVII SEQ ID NO 1.
XX	

KW	Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM	cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Misc-difference
FT	6
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	7
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	14
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	16
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	19
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	20
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	25
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	26
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	29
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	35
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	52
FT	/note= "O-glycosylated"
FT	60
FT	/note= "O-glycosylated"
FT	145
FT	/note= "N-glycosylated"
FT	152..153
FT	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	322
FT	/note= "N-glycosylated"
PN	WO200158935-A2.
XX	
XX	16-AUG-2001.
XX	
XX	12-FEB-2001; 2001WO-DK00094.
XX	
XX	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAYY-) MAYYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaaes C;
XX	
DR	WPI: 2001-581807/65.
XX	
DR	N-PSDB; AA199982.
XX	
PT	New conjugate, useful for treating Factor VIIA related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -
XX	
PS	Claim 1, Page 81-83; 89pp; English.
XX	

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 / Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLRNGLRNGSLRXRCRX.....XXAEXIFRNXXRTRQFWVSY 44

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	77.9	407	1 KFB07	coagulation factor
2	130	68.4	443	2 I46932	coagulation factor
3	122	64.2	466	1 KFH07	coagulation factor
4	108	56.8	461	1 JX0210	protein C (activat
5	107	56.3	461	1 S18994	protein C (activat
6	96	50.5	456	1 KXBO	protein C (activat
7	95	50.0	482	1 EXRT	coagulation factor
8	95	50.0	488	1 EXHU	coagulation factor
9	94	49.5	461	1 KXHU	protein C (activat
10	90	47.4	492	1 EXBO	coagulation factor
11	88	46.3	416	1 KFB0	coagulation factor
12	88	46.3	461	1 KFHU	coagulation factor
13	83	43.7	452	1 A30351	coagulation factor
14	83	43.7	459	2 JQ0419	coagulation factor
15	82	43.2	475	1 EXCH	coagulation factor
16	77	40.5	622	1 TBHU	thrombin (EC 3.4.2
17	75	39.5	642	2 S53433	plasma protein S p
18	74	38.9	617	2 S10511	thrombin (EC 3.4.2
19	74	38.9	618	2 A35827	thrombin (EC 3.4.2
20	71	37.4	675	1 KXBO	plasma protein S p
21	70	36.8	642	2 S53434	plasma protein S p
22	70	36.8	646	2 S38819	plasma protein S p
23	70	36.8	676	1 KXHU	thrombin (EC 3.4.2
24	68	35.8	625	1 TBBO	thrombin (EC 3.4.2
25	68	35.8	675	1 KXRTS	plasma protein S p
26	67	35.3	422	1 KXHU	plasma protein Z p
27	63	33.2	396	1 KXBO	plasma protein Z p
28	61	32.1	675	1 KXMS	plasma protein S p
29	59	31.1	678	2 B48089	growth arrest-spec

30	58	30.5	673	2 A48089	growth arrest-spec
31	56	29.5	413	1 VHVNIH	nucleoprotein - in
32	56	29.5	674	2 I55476	growth potentiatin
33	53	27.9	605	1 MWLEB	El protein - bovin
34	53	27.9	620	1 MWLEB	El protein - bovin
35	49.5	26.1	594	2 D84859	probable MAP kinase
36	49.5	26.1	603	2 C96575	probable MAP kinase
37	49	25.8	1217	2 T21403	hypothetical prote
38	48.5	25.5	576	2 G96763	probable MAP kinase
39	45	23.7	687	2 T08528	probable DNA topoi
40	44	23.2	1101	2 T25919	hypothetical prote
41	43	22.6	219	2 AE2449	hypothetical prote
42	43	22.6	267	2 JC1527	coat protein - pot
43	43	22.6	440	2 C83368	probable MFS trans
44	42.5	22.4	907	2 T15992	hypothetical prote
45	42	22.1	320	2 G84993	glutathione syntha

ALIGNMENTS

RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C/Accession: A31979; C20274

R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A/Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; PMID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <RAK>

R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A/Reference number: A20274; PMID:83308813; PMID:6688526

A/Accession: C20274

A/Molecule type: protein

A/Residues: 58-62, 'X', 64-68 <MCW>

A/Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R/ase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.

J. Biochem. 104, 867-868, 1988

A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A/Reference number: A44556; PMID:89213999; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carbohydrate

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser

gulation factor IX in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F/1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F/1-44/Domain: Gla domain homology (fragment) <GLA>

F/50-81/Domain: EGF homology <EGF>

F/91-127/Domain: EGF homology <EGF>

F/153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F/153-387/Domain: trypsin homology <TRY>

F/6-7-14-16-19-20-25-26-29-34-35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F/17-22-50-61-55-70-72-81-91-102-98-112-114-127-135-262-159-164-178-194-310-329-340-368/I

F/52/Binding site: carboxylate (Ser) (covalent) #status experimental

F/63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F/145-203/Binding site: carboxylate (Asn) (covalent) #status experimental

F/152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental

F/193-242/Cleavage site: His, Asp, Ser #status predicted

F/290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match

Best Local Similarity 77.9%; Score 148; DB 1; Length 407;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

C:Date: 31-Jan-1995 #sequence #revision 07-Feb-1997 #text_change 08-Dec-2000

C:Accession: S49075, J04670, F50191, PS0190, I62745

R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Thromb. Res. 80, 63-73, 1995

A:Title: Evidence for competition between vitamin K-dependent clotting factors for intravascular fibrinogen

A:Accession number: A58498; MUID:96093366; PMID:8578539

A:Accession: S49075

A:Molecule type: mRNA

A:Residues: 1-482 <STA1>

A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:9506601

A:Note: submitted to the EMBL Data Library, June 1994

A:Note: neither the complete nucleic acid sequence nor the complete translation are shown

R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.

Gene 169, 269-273, 1996

A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.

A:Reference number: J04670; MUID:96194815; PMID:8647460

A:Accession: J04670

A:Molecule type: mRNA

A:Residues: 1-482 <STA2>

A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:9506601

A:Experimental source: Cos-1 cell

R:Enjyoji, K.; Miyazaki, K.; Kato, H.

J. Biochem. 109, 890-898, 1991

A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma

A:Reference number: PS0190; MUID:92041742; PMID:1718949

A:Accession: PS0191

A:Molecule type: protein

A:Residues: 41-58, 'X', 60-65 <ENJ1>

A:Accession: PS0190

A:Molecule type: protein

A:Residues: 183-186, 'X', 188-207 <ENJ2>

R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.

Eur. J. Haematol. 52, 162-168, 1994

A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of factor X

A:Reference number: I46196; MUID:94222160; PMID:8168596

A:Accession: I62745

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 295-383, 'G', 385-455 <MUR>

A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396

C:Function:

A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor Va

A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid

R:1-23/Domain: signal sequence #status predicted <STG>

R:24-40/Domain: propeptide #status predicted <PRO>

R:25-84/Domain: Gla domain homology <GLA>

R:41-179/Product: coagulation factor X light chain #status predicted <LCH>

R:120-121/Domain: EGF homology <EG1>

R:129-164/Domain: EGF homology <EG2>

R:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>

R:183-231/Domain: activation peptide #status predicted <APR>

R:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>

R:232-460/Domain: trypsin homology <TRY>

R:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <Glu>

R:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,411-419/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <Glu>

R:103/Modified site: gamma-carboxyglutamic acid (Asp) #status predicted <Asp>

R:187/Binding site: carboxylate (Asn) (covalent) #status experimental

R:208/Binding site: carboxylate (Thr) (covalent) #status predicted

R:218/Binding site: carboxylate (Asn) (covalent) #status predicted

R:231-233/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status predicted

R:274,320,411/Active site: His, Asp, Ser #status predicted

Query Match	50.0%	Score 95	DB 1	Length 482
Best Local Similarity	36.4%	Pred. No. 1.6e-08		
Matches 16	Conservative 8	Mismatches 20	Indels 0	Gaps 0
Qy	1	ANGFLXXLRNGSLRXCRXXLCSPYXAEIIFRNXXRTQRFWSY	44	
Db	41	ANGFFFEIKGNLRRECVCEIICSPFEAREVFEDNEKTTTFWNY	84	

RESULT 8

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N.Alterate names: Stuart factor

C.Species: Homo sapiens (man)

C.Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 08-Dec-2000

C.Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; 154051; A00

R.Riley, S.P.; Foster, D.C.; Kurachi, K.; Dave, E.W.

Biochemistry 25, 5098-5102, 1986

A.Title: Gene for human factor X: a blood coagulation factor whose gene organization is

A.Reference number: A24478; PMID:8702600; PMID:3768336

A.Accession: A24478

A.Molecule type: DNA

A.Residues: 1-488 <LE>

A.Cross-references: GB:U29433; GB:M14327; NID:9459609; PIDN:AAA52764.1; PID:g182831

R.Messler, T.L.; Plutman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A.Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X

A.Reference number: J00917; PMID:91216473; PMID:1992434

A.Accession: J00917

A.Molecule type: mRNA

A.Residues: 1-488 <MES>

A.Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:g182390

R.Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A.Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor

A.Reference number: A42485; PMID:92218390; PMID:1313796

A.Accession: A42485

A.Molecule type: DNA

A.Residues: 1-15 <MIA>

A.Experimental source: liver

A.Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)

R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagdeeswaran, P.

Gene 41, 311-314, 1986

A.Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A.Reference number: A25853; PMID:86221713; PMID:3011603

A.Accession: A25853

A.Molecule type: mRNA

A.Residues: 19-284, 'E', 289-488 <XAU>

A.Cross-references: GB:M2613; NID:9180335; PIDN:AAA51984.1; PID:g180336

R.Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A.Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X

A.Reference number: A22208; PMID:85216545; PMID:2582420

A.Accession: A22208

A.Molecule type: mRNA

A.Residues: 13-441, 'S', 443-488 <FUN>

A.Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:g182841

R.Riley, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A.Title: Characterization of a cDNA coding for human factor X.

A.Reference number: A21284; PMID:84222026; PMID:6587384

A.Accession: A21284

A.Molecule type: mRNA

A.Residues: 13-284, 'E', 289-488 <LE2>

A.Cross-references: GB:K01886

R.McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Saegawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss

Biochemistry 22, 2875-2884, 1983

A.Title: Complete amino acid sequence of the light chain of human blood coagulation factor X

A.Reference number: A20362; PMID:83257207; PMID:6871167

A.Accession: A20362

A.Molecule type: protein

A.Residues: 41-179 <MCW>

R.Inoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A.Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X

A.Reference number: S39414; PMID:94062825; PMID:8234361

A.Accession: S39415

A.Molecule type: protein

A.Residues: 183-234 <INO>

A.Note: glycosylation sites

A.Note: identification and characterization of beta-hydroxyaspartic acid

R.Jagdeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.

Gene 84, 517-519, 1989
 A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: I54051, MUID:90128239; PMID:2612918
 A:Accession: I54051
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:q18360; PIDN:AA52636.1; PID:q553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blä
 J. Mol. Biol. 232, 947-966, 1993
 A>Title: Structure of human dcs(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277; PMID:8355279
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetic:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A:Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <Gla>
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:120-164/Domain: EGF homology <EGF>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <APT>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-63/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.0%; Score 95; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. NO. 1.6e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRCRXXKCSFXAXEJFRNXXRTROFVSV 44
 Db 41 ANSFLEBKXGHLRECEMETCTSYEARREVEDSDKTNEFNK 84

RESULT 9
 KXHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: autoproteobin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 A:Accession: A22331; A25426; A21781; A23789; A00927
 R:Forster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A>Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <ROS1>
 A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A>Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, 'U', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Forster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'Q', 107-461 <ROS2>
 A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and 1t
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Millerich, J.P.; Broeze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
 A:Reference number: A44605; MUID:90293094; PMID:1694179
 A:Contents: annotation; carboxylate binding sites; activation peptide
 A:Note: The alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544994
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine protease that in
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.
 C:Genetic:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <Gla>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EGF>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status experimental <APT>
 F:202-211/Domain: activation peptide #status experimental <ACT>
 F:212-445/Domain: trypsin homology <TRY>
 F:46,49,56,58,61,62,67,68,71/Modified site: gamma-carboxylglutamic acid (Glu) #status exp
 F:59-64,92-105,101-120,122-131,140-151,147-160,163-175,183-319,238-254,373-387,398-426/Di
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Ileu (thrombin) #status experimental
 F:233,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 49.5%; Score 94; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. NO. 2.2e-08;
 Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRCRXXKCSFXAXEJFRNXXRTROFV 41
 Db 43 ANSFLEBKXGHLRECEMETCTSYEARREVEDSDKTNEFNK 83

RESULT 10
 EXBO
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N/Alternate names: Stuart factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 C/Fung: M.R.; Campbell, R.M.; MacGillivray, T.A.
 Nucleic Acids Res. 12: 4481-4492, 1984
 A/Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A/Reference number: A22867; MUID:84247315; PMID:6330671
 A/Accession: A22867
 A/Molecule type: mRNA
 A/Residues: 1-487 <FUN>
 A/Cross-references: GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
 R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A/Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A/Reference number: A14997; MUID:80130563; PMID:6766735
 A/Accession: A14997
 A/Molecule type: protein
 A/Residues: 41-102, 'N', 104-180 <ENF>
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Contents: annotation; revision to residue 103
 R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A/Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A/Reference number: A12030; MUID:76053069; PMID:1059093
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-252,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKRG', 446-492 <T
 A/Note: carboxydrate binding sites and disulfide bonds were determined
 R/Peterson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A/Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A/Reference number: A34412; MUID:89380326; PMID:2789221
 A/Accession: A34412
 A/Molecule type: protein
 A/Residues: 85-126 <PER>
 A/Note: beta-hydroxyaspartic acid site
 R/Moue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39414
 A/Molecule type: protein
 A/Residues: 183-186,199-209,216-233 <IMO>
 A/Note: carboxydrate binding sites
 R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A/Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
 A/Reference number: A12453; MUID:73053114; PMID:4264286
 A/Contents: annotation; active site
 R/Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A/Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
 A/Reference number: A13504; MUID:76053121; PMID:1059122
 A/Contents: annotation; activation
 R/Sugo, T.; Björk, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A/Reference number: A58024; MUID:84185716; PMID:6546930
 A/Contents: annotation; calcium binding
 R/Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A/Reference number: A38025; MUID:86140210; PMID:3948800
 A/Contents: annotation; sulfate binding
 C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with ser
 C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C/Genetics:
 A/Gene: F10
 A/Map position: 13q34
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid, blood coagulation; calcium binding; carboxyglutami
 F/1-15/Domain: signal sequence #status predicted <SIG>
 F/16-40/Domain: propeptide #status predicted <PRO>
 F/41-180/Domain: Gla domain homology <Gla>
 F/90-121/Domain: coagulation factor X light chain #status experimental <LCH>
 F/129-154/Domain: EGF homology <EGF>
 F/183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F/185-233/Domain: activation peptide #status experimental <APR>
 F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AMC>
 F/234-461/Domain: trypsin homology <TRY>
 F/46, 47, 54, 56, 59, 60, 65, 66, 67, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F/57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status pr
 F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F/200/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental
 F/208, 485/Binding site: carboxydrate (Thr) (covalent) #status experimental
 F/218/Binding site: carboxydrate (Asn) (covalent) #status experimental
 F/233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stati
 F/240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental
 F/275, 321, 418/Active site: His, Asp, Ser #status predicted

Query Match 47.4%; Score 90; DB 1; Length 492;
 Best Local Similarity 36.4%; Pred. No. 1.2e-07;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGLKRXCKXXLCSFKYKAEYTRNKKXRTQFVSVY 44
 DB 41 ANSFLEVKQNLRECELEACSLSEAREVEFDEAQTDFMSKY 84

RESULT 11
 KBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N/Alternate names: Christmas factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999
 C/Accession: A14757; B20274; I55891; A00923
 R/Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Tit
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
 A/Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac
 A/Reference number: A14757; MUID:80056619; PMID:291916
 A/Accession: A14757
 A/Molecule type: protein
 A/Residues: 1-63, 'T', 65-416 <KAT>
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Accession: B20274
 A/Molecule type: protein
 A/Residues: 59-63, 'X', 65-69 <MCM>
 R/Choo, K.H.; Gould, K.G.; Rees, D.J.C.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A/Title: Molecular cloning of the gene for human anti-naemophilic factor IX.
 A/Reference number: I45891; MUID:82272386; PMID:6287285
 A/Accession: I45891
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 52-139 <CHO>
 A/Cross-references: GB:U0007; NID:G15053; PIDN:AAA30520.1; PID:G15054
 R/Haee, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S
 J. Biochem. 104, 867-868, 1988
 A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A/Reference number: A44566; MUID:89213999; PMID:3149637
 A/Contents: annotation
 A/Note: structure and location of a carboxydrate covalently bound to Ser

C:Comment: Factor IX is activated by factor XII, which excises the activation peptide p
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pres
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; blood homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; Gln homology; calcium binding; carboxyglutam
F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <GLA>
F:51-82/Domain: EGF homology <EGF>
F:88-124/Domain: EGF homology <EGF>
F:147-181/Domain: activation peptide #status experimental <APT>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-350/Disulfide
F:53/Binding site: carboxylate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 46.3%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 2,3e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRNGSLKRCXXLCSPFXAXEIRNXXRTQFVWSY 44
Db 3 SGKLEFVRGNLERCEKCKECSFEAREVEPTEKTEFKQY 45

RESULT 12
KFMU
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N:Alternate names: antihemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text change 15-Sep-2000
C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20
R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kirsch, K.
Biochemistry 24, 3736-3750, 1985
A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A:Reference number: A00922; PMID:8600558; PMID:2994716
A:Accession: A00922
A:Molecule type: DNA
A:Residues: 1-461 <YOS>
A:Cross-references: GB:K02402; NID:g182612; PIDN:AA59620.1; PID:g182613
R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro
EMBO J. 3, 1053-1060, 1984
A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; PMID:84236100; PMID:6329734
A:Accession: A37570
A:Molecule type: DNA
A:Residues: 1-461 <ANS>
A:Cross-references: GB:K02048
R:Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Brier, E.
Blood 72, 1074-1076, 1988
A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
A:Reference number: A30511; PMID:88327116; PMID:3416069
A:Accession: A30511
A:Molecule type: DNA
A:Residues: 8-24 <REI>
A:Cross-references: EMBL:X55008; NID:g111288; PIDN:CAH38245.2; PID:g4469253
R:Koberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
A:Reference number: A32989; PMID:89311752; PMID:2773937
A:Accession: A32989
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOB>
R:Reisgraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat

A:Reference number: A22673; PMID:85190593; PMID:3857619
A:Accession: A22673
A:Molecule type: mRNA
A:Residues: 1-193 'T', 195-461 <MCG>
A:Cross-references: GB:M11309; NID:g180552; PIDN:AA52023.1; PID:g180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Raye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstoshe
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; PMID:83220788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193 'T', 195-461 <JAG>
A:Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611
R:Jagdeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of a cDNA coding for human factor IX
A:Reference number: A37546; PMID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193 'T', 195-326 <JAG>
A:Cross-references: GB:M35672
R:Kirsch, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; PMID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A', 3
A:Cross-references: GB:J00136; NID:g182608; PIDN:AA58726.1; PID:g182609
A:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; PMID:90194857; PMID:2316207
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
R:McMillen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; PMID:83308813; PMID:6688526
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109, 'X', 111-115 <MCN>
R:Ballard, A.; Faure, T.; Carralio, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle
Eur. J. Biochem. 172, 565-572, 1988
A:Title: Characterization of two differently processed forms of human recombinant factor
A:Reference number: S02527; PMID:8816735; PMID:3280312
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAL>
A:Note: processed forms expressed in recombinant system
R:Ballard, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien, I
EMBO J. 9, 3295-3301, 1990
A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and
A:Reference number: S12058; PMID:9106024; PMID:2209546
A:Accession: S12058
A:Molecule type: mRNA; protein
A:Residues: 1-68 <JAL>
A:Note: processed forms expressed in recombinant system
R:Randford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell
EMBO J. 9, 475-480, 1990
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
A:Reference number: S12377; PMID:90151623; PMID:2406129
A:Accession: S12377
A:Molecule type: protein
A:Residues: 92-130 <HAN>
A:Note: NMR detection of calcium binding by domain expressed in recombinant system
R:de la Salle, C.; Charmanlier, J.L.; Baas, W.C.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
Thromb. Haemost. 70, 370-371, 1993
A:Title: A deletion located in the 3' non translated part of the factor IX gene responsit
A:Reference number: I59612; PMID:94054330; PMID:8236150

A:Accession: 159612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:566752; NID:G439773; PIDN:AA826588.1; PID:G439774
 R:Stoffet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1998
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: 159529; MUID:88127096; PMID:3340835
 A:Accession: 159529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RES>
 A:Cross-references: GB:M19063; NID:G182622; PIDN:AA52456.1; PID:G182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shitomiishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically 11r
 A:Reference number: A54255; MUID:94227047; PMID:812892
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carboxydrat
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carboxydrate binding
 R:McGraw, R.A.; Davie, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding, correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; MUID:86189477; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Stehito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J.
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078229; PMID:2592373
 A:Contents: annotation; sequence of mutant BIM Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor Xla, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C:Genetics:
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <Gla>

F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EG1>
 F:114-170/Domain: EGF homology <EG2>
 F:132-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F:99/Binding site: carboxydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
 F:203,213/Binding site: carboxydrate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carboxydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 46.3%; Score 88; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 2,5e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXLRNGSLXRCXKXLCSPFXAEXIFRNXXRTQFWYSY 44
 Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13

coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: A30351
 A:Reference number: A30351; MUID:89323338; PMID:2752110

A:Title: Molecular cloning of a cDNA encoding canine factor IX.
 A:Reference number: A30351

A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-452 <EVA>

A:Cross-references: GB:M21757; NID:G972719; PIDN:AAJ75006.1; PID:G163948
 R:Axelrod, U.H.; Read, M.S.; Brinkhouse, K.M.; Verm, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990

A:Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic
 A:Reference number: I46201; MUID:90311364; PMID:2367529

A:Accession: I46201
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-452 <AXE>

A:Cross-references: GB:M3826; NID:G163949; PIDN:AAJ0844.1; PID:G163950
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-40/Domain: propeptide #status predicted <PRO>
 F:24-84/Domain: Gla domain homology <Gla>

F:41-45/Product: coagulation factor IX #status predicted <MAT>
 F:90-121/Domain: EGF homology <EG1>

F:127-163/Domain: EGF homology <EG2>
 F:218-445/Domain: trypsin homology <TRY>

F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/D1
 F:258,306,402/Active site: His, Asp, Ser #status predicted

Query Match 43.7%; Score 83; DB 1; Length 452;
 Best Local Similarity 37.2%; Pred. No. 1,8e-06;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXLRNGSLXRCXKXLCSPFXAEXIFRNXXRTQFWYSY 44
 Db 42 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTEFWKQY 84

RESULT 14

coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C/Accession: J00419.1 199667
R/Mu, S.M., Stafford, D.W., Ware, J.
Gene 86, 275-278, 1990
A/Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
A/Reference number: J00419; MWID:90215309; PMID:2323576
A/Accession: J00419
A/Molecule type: mRNA
A/Residues: 1-459 <MUS>
A/Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158
A/Experimental source: liver
R:Sarkar, G.; Koerber, D.D.; Sommer, S.S.
Genomics 6, 133-143, 1990
A/Title: Direct sequencing of the activation peptide and the catalytic domain of the fad
A/Reference number: I46580; MWID:90152675; PMID:2303254
A/Accession: I49667
A/Status: preliminary; translated from GB/EMBL/DBU
A/Molecule type: mRNA
A/Residues: 168-362, 'O', 364-387, 'I', 389-451 <RES>
A/Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320
C/Comment: This protein plays a critical role in blood coagulation.
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F:17-39/Domain: propeptide #status predicted <PRO>
F:19-79/Domain: Gla domain homology <GLA>
F:35-459/Product: coagulation factor IX #status predicted <MAY>
F:85-116/Domain: EGF homology <EG1>
F:122-158/Domain: EGF homology <EG2>
F:225-452/Domain: trypsin homology <TRY>
F:41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #S
F:52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/DLS
F:265,313,409/Active site: His, Asp, Ser #status predicted

Query Match 43.7%; Score 83; DB 2; Length 459;
Best Local Similarity 37.2%; Pred. No. 1.8e-06;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXLRNGSLXRCRXXLCSEFYXAEIIFRNXXRTROFWVSY 44
DB 37 SGKLEFVRGNLRECEERCSFEAREVFENTETKTEPFWKQY 79

RESULT 15

EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N/Alternate names: virus-activating proteinase
C/Species: Gallus gallus (chicken)
C/Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C/Accession: S15838; S20380; S20381
R/Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotch, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991
A/Title: Primary structure of the virus activating protease from chick embryo. Its ident
A/Reference number: S15838; MWID:91257322; PMID:2044767
A/Accession: S15838
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-475 <SUZ>
A/Cross-references: DDBJ:00844; NID:g222869; PIDN:BAA0724.1; PID:g222870
R:Gotch, B.; Yamuchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A/Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsi
A/Reference number: S20380; MWID:92164779; PMID:1537403
A/Accession: S20380
A/Molecule type: protein
A/Residues: 41-55 <GO2>
A/Accession: S20381
A/Molecule type: protein
A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <GO2>
C/Function:
A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:81-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #S
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #S
F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,421
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 43.2%; Score 82; DB 1; Length 475;
Best Local Similarity 34.1%; Pred. No. 2.8e-06;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCRXXLCSEFYXAEIIFRNXXRTROFWVSY 44
DB 41 ANGFLEEMKQGNTERECNEBRCSEAREAFEDNEKTEPFWNJY 84

Search completed: March 19, 2003, 15:00:58
Job time : 30.125 secs

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 seconds

(without alignments)
328.082 Million cell updates/sec

Title: 10ASN28GLU_4

Perfect score: 190

Sequence: 1 ANGFLXLXNLGSLXRCRX.....XXAEXIFRMXXRTRQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	77.9	407	1	FA7_BOVIN
2	130	68.4	407	1	FA7_RABIT
3	122	64.2	466	1	P98139 oryctolagus
4	108	56.8	461	1	TMG1_HUMAN
5	108	56.8	461	1	PRTC_MOUSE
6	107	56.3	461	1	PRTC_RAT
7	105	55.3	446	1	FA7_MOUSE
8	102	53.7	231	1	TMG3_HUMAN
9	101	53.2	459	1	PRTC_PIG
10	96	50.0	488	1	PRTC_BOVIN
11	95	50.0	488	1	FA10_HUMAN
12	94	49.5	461	1	PRTC_HUMAN
13	93	48.9	490	1	FA10_RABIT
14	90	47.4	492	1	FA10_BOVIN
15	88	46.3	461	1	FA9_BOVIN
16	88	46.3	461	1	FA9_HUMAN
17	85	44.7	488	1	PRTC_RABIT
18	83	43.7	452	1	FA9_CANPA
19	83	43.7	459	1	FA9_MOUSE
20	82	43.2	475	1	FA10_CHICK
21	77	40.5	622	1	THRB_HUMAN
22	74	38.9	617	1	THRB_RAT
23	74	38.9	618	1	THRB_MOUSE
24	71	37.4	675	1	PRIS_BOVIN
25	70	36.8	202	1	TMG2_HUMAN
26	70	36.8	226	1	TMG4_HUMAN
27	70	36.8	646	1	PRTS_RABIT
28	70	36.8	649	1	PRTS_HUMAN
29	70	36.8	676	1	PRTS_HUMAN
30	68	35.8	376	1	FA10_TROCA
31	68	35.8	625	1	THRB_BOVIN
32	68	35.8	675	1	PRTS_RAT
33	67	35.3	400	1	PRTZ_HUMAN

34	63	33.2	396	1	PRTZ_BOVIN
35	61	32.1	675	1	PRTS_MOUSE
36	56	29.5	413	1	NCAPI_HNV
37	53	27.9	604	1	VE1_BPV2
38	53	27.9	605	1	VE1_BPV1
39	45	23.7	818	1	CDB1_HUMAN
40	45	22.6	350	1	V0D1_DROME
41	42	22.1	320	1	GSHB_BUCA
42	42	22.1	473	1	AM13_MYCTU
43	42	22.1	473	1	FP2_MYCTU
44	42	22.1	484	1	SLF2_YEAST
45	42	22.1	1275	1	RFBC_MYXXA

ALIGNMENTS

RESULT 1	ID	FA7_BOVIN	STANDARD;	PRT;	407 AA.
AC	P22457;				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).				
DE	accelerator).				
GN	F7.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=69008362; PubMed=3049594;				
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,				
RA	Iwanaga S.;				
RT	"Bovine factor VII. Its purification and complete amino acid				
RT	sequence.";				
RL	J. Biol. Chem. 263:14868-14877(1988).				
RN	[2]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.				
RX	MEDLINE=91344709; PubMed=2129367;				
RA	Iwanaga S., Nishimura H., Kawabata S., Kisei W., Hase S., Ikenaka T.;				
RT	"A new trisaccharide sugar chain linked to a serine residue in the				
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";				
RL	Adv. Exp. Med. Biol. 281:121-131(1990).				
CC	- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOSEN FORM. FACTOR VII IS				
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIIA, FACTOR IXA, OR				
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR				
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA				
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO				
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.				
CC	- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to				
CC	form factor Xa.				
CC	- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED				
CC	BY A DISULFIDE BOND.				
CC	- TISSUE SPECIFICITY: PLASMA.				
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME				
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND				
CC	CALCIUM.				
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.				
DR	PIR; A31979; A31979.				
DR	HSSP; P08709; 1BF9.				

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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT BINDING 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
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FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
Query Match 77.9%; Score 148; DB 1; Length 407;
Beet Local Similarity 68.2%; Pred. No. 2,3e-19;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 ANGFLXLRNGSLRXKCRXXICSTFYXAEKIRNXXRTROFVASY 44
Db 1 ANGFLXELPLGSLRECRECELCSFEAEHIFRNERTRQFVASY 44

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
ID FA7_RABIT
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch).
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EMBL; U77477; BAB37326.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.

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DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF CA; 1.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYP SIN DOM; 1.
 DR PROSITE; PS00134; TRYP SIN HIS; 1.
 DR PROSITE; PS00135; TRYP SIN SER; 1.
 KM Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KM EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 39 POTENTIAL.
 FT CHAIN 40 191 FACTOR VII LIGHT CHAIN.
 FT CHAIN 192 444 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 45 74 GLA-RICH.
 FT DOMAIN 85 121 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 126 167 EGF-LIKE 2.
 FT DOMAIN 192 444 SERINE PROTEASE.
 FT SITE 191 192 CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 FT ACT_SITE 281 281 BY SIMILARITY.
 FT ACT_SITE 383 383 BY SIMILARITY.
 FT BINDING 377 377 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 56 61 BY SIMILARITY.
 FT DISULFID 89 100 BY SIMILARITY.
 FT DISULFID 94 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 130 141 BY SIMILARITY.
 FT DISULFID 137 151 BY SIMILARITY.
 FT DISULFID 153 166 BY SIMILARITY.
 FT DISULFID 174 301 BY SIMILARITY.
 FT DISULFID 198 203 BY SIMILARITY.
 FT DISULFID 217 233 BY SIMILARITY.
 FT DISULFID 349 368 BY SIMILARITY.
 FT DISULFID 379 407 BY SIMILARITY.
 FT MOD_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 102 102 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 444 AA; 49011 MW; 0481ABCF5427F8 CRC64;

Query Match 68.4%; Score 130; DB 1; Length 444;
 Best Local Similarity 52.3%; Prec. No. 4.9e-16;
 Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

01 ANGFLXXLRNGSLKRXCRXXKCSFXKXEIFRNXXKTRQFVSVY 44
 40 ANSPLEELRPGSLERCKEELCSFEAREVQSTERTQFWITY 83

RESULT 3
 PAF HUMAN STANDARD; PRT; 466 AA.
 AC P08709; Q14339;
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator) (Eptacog alfa).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86205965; PubMed=3486420;
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
 RA Davie E.W.;
 RT "Characterization of a cDNA coding for human factor VII."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260948; PubMed=3037537;
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
 RA Hagen F.S., Murray M.J.;
 RT "Nucleotide sequence of the gene coding for human factor VII, a
 RT vitamin K-dependent protein participating in blood coagulation."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
 RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=89088153; PubMed=3264725;
 RA Talm L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
 RA Pedersen A.H., Hedner U.;
 RT "Amino acid sequence and posttranslational modifications of human
 RT factor VIIa from plasma and transfected baby hamster kidney cells."
 RL Biochemistry 27:7785-7793(1988).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
 RX MEDLINE=91250411; PubMed=1904059;
 RA Bjorn S., Foster D.C., Thim L., Woberg F.C., Christensen M.,
 RA Komiyama Y., Pedersen A.H., Kistiel W.;
 RT "Human plasma and recombinant factor VII. Characterization of O-
 RT glycosylations at serine residues 52 and 60 and effects of site-
 RT directed mutagenesis of serine 52 to alanine."
 RL J. Biol. Chem. 266:11051-11057(1991).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
 RA Shimomishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z."
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z."
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., P'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kitchener D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor."
 RL Nature 380:41-46(1996).

[9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RP MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 inhibited with a Bp1 mutant."; *J. Mol. Biol.* 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 factor VII."; *Biochemistry* 37:10605-10615(1998).
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 molecule with reduced activity isolated from a clinically unaffected
 male."; *Blood* 78:132-140(1991).
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casenato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 polymorphism in the factor VII gene (F7)."; *Hum. Genet.* 89:497-502(1992).
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 (115His and 333Ser) in the human coagulation factor VII gene."; *Hum. Mol. Genet.* 2:1055-1056(1993).
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunkey H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 polymorphism (SSCP) analysis in five dysfunctional variants of
 coagulation factor VII."; *Hum. Mol. Genet.* 2:1355-1359(1993).
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 cleavage site for activation and altering binding to tissue factor."; *Blood* 83:3524-3535(1994).
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Caecaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodighiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 factors VII (294Ala-->Val) and X (334Ser-->Pro)."; *Hum. Mol. Genet.* 3:1175-1177(1994).
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arfink A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 deficiency causes defective secretion of the molecule."; *Blood* 87:5085-5094(1996).
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Caecaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodighiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8893260;
 RA Tamary H., Fromovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Koroletchevsky M.,
 RA Zaitov R., Seligson U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 deficiency in Moroccan and Iranian Jews."; *Thromb. Haemost.* 76:283-291(1996).
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -I- TISSUE SPECIFICITY: PLASMA.
 CC -I- PMM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query March 64.2%; Score 122; DB 1; Length 466;
 Best local similarity 52.3%; Pred. No. 1.5e-14;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGLSKRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44
 Db 61 ANAFLEELRPSGLRECKEEOCSFEAREIRFKDAERTLFWISY 104

RESULT 4
 TMG1_HUMAN STANDARD; PRT; 218 AA.
 ID O14658;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 DE 1).
 GN PRG1 OR TMG1 OR PRGPI.
 OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; 1CFH.
DR Genew; HGNC:9469; PRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FW PROPP 1 20
FW CHAIN 21 218
FT FT 21 83 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 84 106 POTENTIAL.
FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 61 GLA-RICH.
FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AB98 CRC64;

Query Match 56.8%; Score 108; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 2.5e-12;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANGFLLKRLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTFQWVS 44
Db 21 ANGFPEIRGNIERCKEFCFEAREAFENNEKTKERFWS 64

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RT "Isolation and characterization of a mouse protein C cDNA."
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Svj.
RX MEDLINE=98152576; PubMed=9493582;
RA Jabelt L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
anticoagulant protein C."
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RA Murekawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihio Y.;
RT "A comparative study of partial primary structures of the catalytic
region of mammalian protein C."
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and Villa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECOGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; DA3755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
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FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MM; 53PRA0D85194D6E CRC64;

Query Match 56.8%; Score 108; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 5,4e-12;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

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DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650.
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.,
RT "The cDNA cloning and mRNA expression of rat protein C.",
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64336; CAA45617.1; -.
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; Aex_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

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DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT PROPEP 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 254 254
 FT ACT_SITE 300 300
 FT ACT_SITE 402 402
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 320
 FT DISULFID 239 255
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 215 215
 FT CARBOHYD 291 291
 FT CARBOHYD 355 355
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDAC5 CRC64;

Query Match 56.3%; Score 107; DB 1; Length 461;
 Best local Similarity 45.5%; Pred. No. 8.3e-12;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLLRNGSLKRXCRXXLCSEXXAEXIFRXKXRRPQVSVY 44
 DB 42 ANSFLEVRAGSLERECMEBICDFEEAOEIFQVNEVDLAFWIKY 85

RESULT 7
 ID_FAT_MOUSE STANDARD; PRT; 446 AA.
 AC P70375;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 conversion accelerator).
 GN F7 OR CF7.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97127167; PubMed:8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemostasis. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BP9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vitr_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT CHAIN 194 446
 FT DOMAIN 47 76
 FT DOMAIN 76 76

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FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 128 169 EGF-LIKE 2,
FT DOMAIN 194 446 SERINE PROTEASE.
FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIa,
  FACTOR IXa, OR THROMBIN) (BY SIMILARITY).
FT ACT_SITE 234 234 BY SIMILARITY.
FT ACT_SITE 283 283 BY SIMILARITY.
FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
FT DISULFID 113 122 BY SIMILARITY.
FT DISULFID 132 143 BY SIMILARITY.
FT DISULFID 139 153 BY SIMILARITY.
FT DISULFID 155 168 BY SIMILARITY.
FT DISULFID 176 303 BY SIMILARITY.
FT DISULFID 200 205 BY SIMILARITY.
FT DISULFID 219 235 BY SIMILARITY.
FT DISULFID 351 370 BY SIMILARITY.
FT DISULFID 381 409 BY SIMILARITY.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 446 AA; 50276 MM; 2512E44A5C8C96E CRC64;

Query Match 55.3%; Score 105; DB 1; Length 446;
Best Local Similarity 47.7%; Pred. No. 1.9e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCXRLCSFXAXEIPRNXXRTQFWVSY 44
Db 42 ANSLLEELPQSLERECNEBOCSFEARITFSPERTKQFWIV 85

RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RA MEDLINE=2117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
  proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL AF326350; AA00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
  PROTEIN 3.
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
FT TRANSME 79 101 POTENTIAL.
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MM; 8A37E4848490D81 CRC64;

Query Match 53.7%; Score 102; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.4e-11;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCXRLCSFXAXEIPRNXXRTQFWVSY 44
Db 20 ANFLLELRQGTIERECMEICISIEYKVEVENEKTFPKGY 63

RESULT 9
ID_PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
  factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RA MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
  Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
  protein modeling of membrane binding sites and comparative anatomy of
  domains.";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
  regulates blood coagulation by inactivating factors Va and VIIIa
  in the presence of calcium ions and phospholipide.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
  and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
  into a light chain and a heavy chain held together by a disulfide
  bond. The enzyme is then activated by thrombin, which cleaves a
  tetradecapeptide from the amino end of the heavy chain; this
  reaction, which occurs at the surface of endothelial cells, is
  strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
  residues allows the modified protein to bind calcium.
CC -----
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FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	112	112	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	ACT_SITE	255	255	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	301	301	CHARGE RELAY SYSTEM.
FT	ACT_SITE	400	400	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	CHARGE RELAY SYSTEM.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	321	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	240	256	BY SIMILARITY.
FT	DISULFID	371	385	BY SIMILARITY.
FT	DISULFID	396	424	BY SIMILARITY.
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	459 AA;	51866 MW;	8541AAC14CC16D09 CRC64;

Query Match Best Local Similarity 53.2%; Score 101; DB 1; Length 459; Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0

Qy	1	ANGFLXLRNGSLKXRCXXLCSFYXAEKIFRNXXRTQFWVSY	44
Db	42	ANSFLKEURPSSLERCKEFTCDFEAEAEIPONTENTMAFWMSKY	85

RESULT 10

ID	PRIC_BOVIN	STANDARD;	PRT;	456 AA.
AC	P00745;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)			
DE	(Antithrombin III) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).			
GN	PROC.			
OC	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014826; PubMed=6091100;			
RA	Long G.L., Balagaje R.M., McGillivray R.T.A.;			
RT	"Cloning and sequencing of liver cDNA coding for bovine protein C.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).			
RN	[2]			
RP	SEQUENCE OF 40-194.			
RX	MEDLINE=83007325; PubMed=6896876;			
RA	Fernlund P., Stenflo J.;			
RT	"Amino acid sequence of the light chain of bovine protein C.,"			
RL	J. Biol. Chem. 257:12170-12179(1982).			
RN	[3]			
RP	REVISION TO 110.			
RX	MEDLINE=83169769; PubMed=6572939;			
RA	Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;			
RT	"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).			
RN	[4]			
RP	SEQUENCE OF 197-456.			
RX	MEDLINE=83007326; PubMed=6896877;			
RA	Stenflo J., Fernlund P.;			
RT	"Amino acid sequence of the heavy chain of bovine protein C.,"			
RL	J. Biol. Chem. 257:12180-12190(1982).			

RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.E., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 domainless protein C";
 RL J. Biol. Chem. 258:5548-5553 (1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 by Ca2+ binding to a high affinity site that does not contain gamma-
 carboxyglutamic acid";
 RL J. Biol. Chem. 258:5554-5560 (1983).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 ANOTHER SITE. BEYOND THE GLA DOMAIN, THIS GLA-INDEPENDENT BINDING
 SITE IS NECESSARY FOR THE RECOGNITION OF THE
 THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K02435; AAA0685.1; -.
 DR PIR; A00928; KXBO.
 DR HSSP; P04070; 1PCU.
 DR MEROPS; S01.218; -.
 DR InterPro; IPR000152; Axx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; Gla; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT NON_TER 1 29
 FT SIGNAL <1 1
 FT PROPEP 30 39

FT CHAIN 40 194
 FT PEPTIDE 197 210
 FT DOMAIN 197 210
 FT DOMAIN 94 129
 FT DOMAIN 133 173
 FT DOMAIN 211 456
 FT MOD_RES 45 45
 FT MOD_RES 46 46
 FT MOD_RES 46 46
 FT MOD_RES 53 53
 FT MOD_RES 55 55
 FT MOD_RES 58 58
 FT MOD_RES 59 59
 FT MOD_RES 62 62
 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 110 110
 FT ACT_SITE 252 252
 FT ACT_SITE 298 298
 FT ACT_SITE 397 397
 FT ACT_SITE 56 61
 FT DISULFID 89 103
 FT DISULFID 98 108
 FT DISULFID 102 102
 FT DISULFID 119 128
 FT DISULFID 137 148
 FT DISULFID 144 152
 FT DISULFID 159 172
 FT DISULFID 180 318
 FT DISULFID 237 253
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 FT DISULFID 421 421
 FT CARBOHYD 136 136
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 FT CARBOHYD 366 366
 FT VARIANT 82 82
 FT CONFLICT 455 456
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 Query Match 50.5%; Score 96; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 8.4e-10;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 Qy 1 ANGFLXLRLNRSGLKRXCRXXLCSFYXAEIIFRNXXRTQFWVS 44
 Db 40 ANSFLEELRPGNVERECSEBVCFEFEAREIFQNTDTWAFWSFY 83
 RESULT 11
 ID FA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; O14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 human coagulation factor X.";
 RL Gene 99:291-294 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;

RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C."; 25:5098-5102(1986).
 RL Biochemistry 25:5098-5102(1986).
 RN (13)
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillyray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN (14)
 RP SEQUENCE OF 19-488 FROM N.A.
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN (15)
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasaagawa T., Howald W.N.,
 RA Kwa B.Y., Weinstein B.;
 RT "Complete amino acid evidence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN (16)
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN (17)
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (18)
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128259; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusan K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN (19)
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN (110)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoro H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; K03194; AAA52490.1; -;
 DR EMBL; M57285; AAA52421.1; -;
 DR EMBL; L29433; AAA52764.1; -;
 DR EMBL; L00390; AAA52764.1; JOINED.
 DR EMBL; L00391; AAA52764.1; JOINED.
 DR EMBL; L00392; AAA52764.1; JOINED.
 DR EMBL; L00393; AAA52764.1; JOINED.
 DR EMBL; L00394; AAA52764.1; JOINED.
 DR EMBL; L00395; AAA52764.1; JOINED.
 DR EMBL; L00396; AAA52764.1; JOINED.
 DR EMBL; M22613; AAA51984.1; -;
 DR EMBL; K01886; AAA52486.1; -;
 DR EMBL; M33297; AAA52636.1; -;
 DR PIR; A00924; EXHU.
 DR PIR; A25853; A25853.
 DR PIR; A24478; A24478.
 DR PDB; 1HCG; 08-MAY-95.
 DR PDB; 1FAX; 29-OCT-97.
 DR PDB; 1FXY; 17-JUN-98.
 DR PDB; 1XKA; 23-MAR-99.
 DR PDB; 1XKB; 23-MAR-99.
 DR MEROPS; S01.216; -;
 DR GlycoSuiteDB; P00742; -.
 DR Genew; HGNC:3528; F10.
 DR MIM; 134530; -.
 DR MIM; 227600; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS0186; EGF_2; 2.
 DR PROSITE; PS0187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HTS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydrolyase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31 POTENTIAL.

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FT CHAIN        41      179
FT CHAIN      183      488
FT PROPEP     183     234
FT CHAIN      235     488
FT DOMAIN      86     122
FT DOMAIN     125     165
FT DOMAIN     235     488
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FT MOD_RES     54      54
FT MOD_RES     56      56
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FT MOD_RES     66      66
FT MOD_RES     69      69
FT MOD_RES     72      72
FT MOD_RES     79      79
FT MOD_RES    103     103
FT CARBOHYD    199     199
FT CARBOHYD    211     211
FT CARBOHYD    221     221
FT CARBOHYD    231     231
FT ACT_SITE    276     276
FT ACT_SITE    322     322
FT ACT_SITE    419     419
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FT DISULFID     95     110
FT DISULFID    112     121
FT DISULFID    129     140

Query March 50.0%; Score 95; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 1,4e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

1 ANGFLXLRLNGSLKRXCRXXLCSPYXAEKXIFRNXXRTQFWVSY 44
41 ANSFLEBKMKGHLEKRECHMETCSYEAREVFEFSDKTNMFNMY 84

RESULT 12
PRTC HUMAN STANDARD; PRT; 461 AA.
ID P04070; Q16001; Q15190; Q15189;
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Anticlotting protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Santeiro R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J., Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translocation may influence the frequency of usage at asparagine-X-
RT cytosine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Eamon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Glu-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Haasan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=9008906; PubMed=2602169;
RA Grundy C.B., Chitcliffe A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGC-->TGC) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]

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RP VARIANT CVS-272.
 RX MEDLINE=91329836; PubMed=1868249;
 RA Reitsma P.H., Poort S.R., Allaart C.F., Brier E., Bertina R.M.;
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with
 RT symptomatic protein C deficiency type I: heterogeneity and founder
 RT effects.";
 RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Ralville I.R., Long G.L.;
 RT "Protein C deficiency: symptomatic type II protein C deficiency
 RT associated with two Glu domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schullman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandtillie S., Vidau M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwasaaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CVS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gandtillie S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
 RA Juhani-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]

RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignelli P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Glu domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous
 RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard U.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrachini P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 QY 1 ANGFLXLRNGSLRXRCRXKCSFXAXEYFRMXXTROFW 41
 Db 43 ANSFLELRHSLERECIEBICFPEAKEIFQVDDTLFW 83
 AC 019045; STANDARD; PRT; 490 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X.";
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.


```

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CC -----
DR EMBL: AF003200; AAB62542.1; -.
DR HSSP: P00742; IHCG.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Aex_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin. 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00179; EGF_CA. 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Src; 1.
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DR PROSITE: PS01186; EGF_2; 2.
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DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR GlycoProtein: Hydroxylase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20
FT PROPEP 21 40
FT CHAIN 41 180
FT PROPEP 184 490
FT PROPEP 184 232
FT CHAIN 233 490
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 233 490
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 56 56
FT MOD_RES 59 59
FT MOD_RES 60 60
FT MOD_RES 65 65
FT MOD_RES 66 66
FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 75 75
FT MOD_RES 79 79

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FT MOD_RES 103 103
FT ACT_SITE 274 274
FT ACT_SITE 320 320
FT ACT_SITE 417 417
FT DISULFID 90 101
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140
FT DISULFID 136 149
FT DISULFID 151 164
FT DISULFID 172 340
FT DISULFID 239 244
FT DISULFID 259 275
FT DISULFID 388 402
FT DISULFID 413 441
FT CARBOHYD 61 61
FT CARBOHYD 187 187
FT CARBOHYD 205 205
SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 48.9%; Score 93; DB 1; Length 490;
Best Local Similarity 38.6%; Pred. No. 3.2e-09;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLKRCXKXLCSEFXAXEIPRNXXRTQFNVS 44
Db 41 ANSFLEELKGNLRECHWENCSEYEALEVEDREKTFNWKY 84

RESULT 14
P10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
[1]
SEQUENCE OF 1-487 FROM N.A.
MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
[2]
SEQUENCE OF 41-180.
MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor)."
RL Biochemistry 19:659-667(1980).
[3]
REVISION TO 103.
MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
[4]
SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."

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Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 (5)
 SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 MEDLINE=94062825; PubMed=8243461;
 Inoue K., Morita T.;
 "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X." The role of the carbohydrate
 RT moieties in the activation of factor X.";
 Eur. J. Biochem. 218:153-163(1993).
 (6)
 ACTIVE SITE
 MEDLINE=7305314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 Biochemistry 11:4899-4903(1972).
 (7)
 PROCESSING.
 MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 (8)
 CALCIUM-BINDING DATA.
 MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 J. Biol. Chem. 259:5705-5710(1984).
 (9)
 SULFATION.
 MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 J. Biol. Chem. 261:4008-4014(1986).
 (10)
 STRUCTURE BY NMR OF 85-126.
 MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 Biochemistry 29:8111-8118(1990).
 (11)
 STRUCTURE BY NMR OF 85-126.
 MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 Biochemistry 31:5974-5983(1992).
 (12)
 STRUCTURE BY NMR OF 85-126.
 MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 J. Biol. Chem. 267:19642-19649(1992).
 (13)
 STRUCTURE BY NMR OF 41-126.
 MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC convert prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A00925; EXBO.
 CC PDB; IAPQ; 31-JAN-94.
 CC PDB; ICCF; 31-MAY-94.
 CC PDB; 1MHE; 15-MAY-97.
 CC PDB; 1MHP; 15-MAY-97.
 CC MEROPS; S01.216; -.
 CC DR GlycosultedB; P00743; -.
 CC DR InterPro; IPR000152; Asx hydroxyl.
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR007042; EGF_2.
 CC DR InterPro; IPR001881; EGF_Ca.
 CC DR InterPro; IPR002383; GLA_blood.
 CC DR InterPro; IPR001254; Ser_protease_Try.
 CC DR InterPro; IPR000294; VitK_dep_GLA.
 CC DR Pfam; PF00008; EGF_2.
 CC DR Pfam; PF00089; trypsin; 1.
 CC DR Pfam; PF00594; gla; 1.
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.
 CC DR PRINTS; PR00001; GLABLOOD.
 CC DR SMART; SM00179; EGF_CA; 1.
 CC DR SMART; SM00001; EGF_like; 1.
 CC DR SMART; SM00069; GLA; 1.
 CC DR SMART; SM00020; TRYP_SPC; 1.
 CC DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; 2.
 CC DR PROSITE; PS01187; EGF_CA; 1.
 CC DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC FT SIGNAL 1 23
 CC FT PROPEP 24 40
 CC FT CHAIN 41 180
 CC FT CHAIN 183 492
 CC FT PROPEP 183 233
 CC FT CHAIN 234 492
 CC FT PROPEP 476 492
 CC FT DOMAIN 86 122
 CC EGF-like 1, CALCIUM-BINDING (POTENTIAL).
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR Xa, HEAVY CHAIN.
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR
 CC ACTIVATION.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT SITE 275 275 CHARGE RELAY SYSTEM.
FT ACT SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 47.4%; Score 90; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 1,1e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCXKXLCSPFXAXEIRNXXRTQFWVS 44
Db 41 ANSFLXEVKQGNLERECLEACSLSEAREVEFEDAQDFWFSKY 84

RESULT 15
FA9_BOVIN STANDARD; PRT; 416 AA.
AC P00741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80056619; PubMed=291916;
RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
RA Davie E.W., Tiltam K.;
RT "Comparison of amino acid sequence of bovine coagulation factor IX
RT (Christmas factor) with that of other vitamin K-dependent plasma
RT proteins";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
RN [2]
RP REVISION TO 64.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [3]
RP SEQUENCE OF 51-111 FROM N.A.
RX MEDLINE=82272386; PubMed=6287289;
RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
RT "Molecular cloning of the gene for human anti-haemophilic factor IX.";
RL Nature 299:178-180(1982).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimomichi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX.";
RL J. Biochem. 104:867-868(1988).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
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RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90130422; PubMed=2105311;
RA Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
RT "The structure of (xylose)2glucose-O-serine 53 found in the first
RT epidermal growth factor-like domain of bovine blood clotting factor
RT IX.";
RL J. Biol. Chem. 265:1858-1861(1990).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION -
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS. PHOSPHOLIPIDS, AND FACTOR VIIIA.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE
CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
CC BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL, J00007; AAA30520.1; -.
CC PIR, A00923; KFB0.
CC HSSP, P00740; 1CFH.
CC MEROPS, S01.214; -.
CC GlycoSiteDB: P00741; -.
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000742; EGF 2.
CC InterPro: IPR001881; EGF Ca.
CC InterPro: IPR001438; EGF II.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR001254; Ser_protease_Try.
CC InterPro: IPR000294; VitK_dep_GLA.
CC Pfam: PF00008; EGF; 2.
CC Pfam: PF00089; trypsin; 1.
CC Pfam: PF00594; gla_1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00010; EGFBL00D.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00179; EGF_CA; 1.
CC SMART: SM00001; EGF_like; 1.
CC SMART: SM00069; GLA; 1.
CC SMART, SM00020; Tryp_Sec; 1.
CC PROSITE, PS00010; ASX_HYDROXYL; 1.
CC PROSITE, PS00022; EGF_1; 1.
CC PROSITE, PS01186; EGF 2; 2.
CC PROSITE, PS01187; EGF_CA; 1.
CC PROSITE, PS00011; TRYF_CARBOXYLATION; 1.
CC PROSITE, PS0240; TRYFSIN_DOM; 1.
CC PROSITE, PS00134; TRYFSIN_HIS; 1.
CC PROSITE, PS00135; TRYFSIN_SER; 1.
CC Blood coagulation; Plasma; Serine protease; Calcium-binding;
CC Hemophilic; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;
CC Hemophilic; Hydroxylation; zymogen; EGF-like domain.
CC CHAIN 1 146 FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
CC PROPEP 147 181 ACTIVATION PEPTIDE.
CC CHAIN 182 416 FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
CC DOMAIN 47 83 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
CC DOMAIN 84 125 EGF-LIKE 2.
CC DOMAIN 182 416 SERINE PROTEASE.
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FT SITE 146 147 CLEAVAGE (BY FACTOR XIA).
FT SITE 181 182 CLEAVAGE (BY FACTOR XIA).
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 8 8 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 HYDROXYLATION.
FT DISULFID 18 23 BY SIMILARITY.
FT DISULFID 51 62 BY SIMILARITY.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 88 99 BY SIMILARITY.
FT DISULFID 95 109 BY SIMILARITY.
FT DISULFID 111 124 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLC. .).
FT CARBOHYD 158 158 /FTID=CAR_000008.
FT CARBOHYD 168 168 N-LINKED (GLCNAC. .).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .).
FT ACT_SITE 222 222 N-LINKED (GLCNAC. .).
FT ACT_SITE 270 270 CHARGE RELAY SYSTEM.
FT ACT_SITE 366 366 CHARGE RELAY SYSTEM.
FT VARIANT 64 64 D -> T (IN REF. 1).
SQ SEQUENCE 416 AA; 46785 MW; 34A7DFB916330662 CRC64;

Query Match 46.3%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 2.2e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXKLNGSLKRXCRXXLCSFYKXAEIIRNXXRTROPWVSY 44
DB 3 SGLKEFVRGNLBERECKEKCSFEAREVPEVNTETKTEFWKQY 45

Search completed: March 19, 2003, 14:52:56
Job time : 6.625 secs

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLLXNGSLXRCRX...XXAEXIFRNXXRTQFWSEY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_protist:*
11: sp_riccia:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvlnus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	64.2	701	1	Q96P08
2	108	56.8	460	11	Q91WN8
3	105	55.3	446	11	Q61109
4	102	53.7	460	11	Q99PC6
5	99	52.1	456	6	Q9TTR0
6	95	50.0	482	11	Q63207
7	92	48.4	481	11	Q54740
8	92	48.4	481	11	Q99J32
9	92	48.4	481	11	Q88947
10	88	46.3	456	6	Q95ME8
11	88	46.3	456	6	Q14316
12	88	46.3	461	6	Q95ND7
13	88	46.3	461	6	Q95ND6
14	88	46.3	469	6	Q9GMD9
15	81	42.6	138	6	Q28994
16	81	42.6	433	13	Q90YK1

17	77	40.5	100	4	Q15253	Q15253 homo sapien
18	77	40.5	608	13	Q9PTW7	Q9PTW7 struthio ca
19	75	39.5	648	6	Q29094	Q29094 sus scrofa
20	74	38.9	399	11	Q9COW3	Q9COW3 mus musculus
21	71.5	37.6	542	5	Q8TE13	Q8TE13 halocynthia
22	70	36.8	179	4	Q8TAS3	Q8TAS3 homo sapien
23	70	36.8	198	11	Q8R182	Q8R182 mus musculus
24	70	36.8	650	4	Q9NSD0	Q9NSD0 homo sapien
25	70	36.8	650	4	Q16519	Q16519 homo sapien
26	65	34.2	607	13	Q91001	Q91001 gallus gall
27	59	31.1	678	4	Q14393	Q14393 homo sapien
28	58	30.5	673	11	Q61592	Q61592 mus musculus
29	58	30.5	674	11	Q99K57	Q99K57 mus musculus
30	57	30.0	95	11	Q9QVH6	Q9QVH6 rattus sp.
31	56	29.5	28	13	P82807	P82807 notechis sc
32	56	29.5	674	11	Q63772	Q63772 rattus sp.
33	56	29.5	674	11	Q98S05	Q98S05 gasterosteus
34	53	27.9	472	13	Q98S06	Q98S06 gasterosteus
35	53	27.9	613	13	Q98S06	Q98S06 gasterosteus
36	50.5	26.6	575	10	Q94E17	Q94E17 oryza sativ
37	50.5	26.6	608	10	Q9XF36	Q9XF36 medicago sa
38	49.5	26.1	196	10	Q04284	Q04284 selaginella
39	49.5	26.1	567	10	Q8W4J2	Q8W4J2 arabidopsis
40	49.5	26.1	603	10	Q9LPG7	Q9LPG7 arabidopsis
41	49.5	26.1	606	10	Q9SUG9	Q9SUG9 arabidopsis
42	49.5	26.1	651	10	Q8S218	Q8S218 oryza sativ
43	49	25.8	1217	5	Q9XV62	Q9XV62 caenorhabdi
44	48.5	25.5	431	10	Q94EY5	Q94EY5 arabidopsis
45	48.5	25.5	492	10	Q9SMJ7	Q9SMJ7 cicor aricet

ALIGNMENTS

RESULT 1

Q96P08 PRELIMINARY; PRT; 701 AA.
ID Q96P08
AC Q96P08
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant Immunocoujugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAKS686.1; -;
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR00742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 64.2%; Score 122; DB 4; Length 701;
 Best Local Similarity 52.3%; Pred. No. 8.2e-14;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTQFWVSY 44
 Db 61 ANAFLEELRPGSLERECNEQCSFEAREIFDAERTKLFWISY 104

RESULT 2

ID 091NM8 PRELIMINARY; PRT; 460 AA.
 AC 091NM8.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strauberg R;
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013896; AAH13896.1; -.
 DR MGD; MGI:97771; Proc.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 56.8%; Score 108; DB 11; Length 460;
 Best Local Similarity 45.5%; Pred. No. 2.1e-11;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTQFWVSY 44
 Db 42 ANSFLEMRPGSLERECMEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 3

ID 061109 PRELIMINARY; PRT; 446 AA.
 AC 061109.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Coagulation factor VII.
 GN F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idnogaite E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY

CC EMBL; U44795; AAC52570.1; -.

DR HSSP; P08709; IFK.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001064; Cysteallin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00659; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BBFDA6870 CRC64;

Query Match 55.3%; Score 105; DB 11; Length 446;
 Best Local Similarity 47.7%; Pred. No. 7.3e-11;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTQFWVSY 44
 Db 42 ANSLLEELMPGSLERECNEQCSFEAREIFKSPERTQFWIVY 85

RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.
 AC 099PC6.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Kott I.;

RT "Complete sequence of UC72A01.",
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY
 DR EMBL: AF318182; AK07918.1; -.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR MGD: MGI:97771; Piroc.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00001; EGF_like_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 DR Hydroxylation; Repeat; Serine protease.
 DR SQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
 SQ
 Query Match 53.7%; Score 102; DB 11; Length 460;
 Best Local Similarity 43.2%; Pred. No. 2,7e-10;
 Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRNGSLKRCXXKCSFXKAEIIFRNXXRTROFVSVY 44
 DB 42 ANSFLIEMRPGSLERECMEIEICDLEAQEIFQNVEDTLAIWIKY 85
 RESULT 5
 Q9TRRO PRELIMINARY; PRT; 456 AA.
 AC Q9TRRO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Protein C precursor.
 GN PROC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunberg L.,
 RT "Molecular characterization and chromosomal assignment of the canine
 RT protein C gene."
 RL Mamm. Genome 10:135-139(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99371952; PubMed=10443005;
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breen B.,
 RT "Analysis of canine protein C gene polymorphisms."
 RL Anim. Genet. 30:237-238(1999).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

DR EMBL: A0001979; CA05126.1; -.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 DR Hydroxylation; Repeat; Serine protease; Signal.
 DR SIGNAL 42
 FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
 FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
 SQ SQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;
 SQ
 Query Match 52.1%; Score 99; DB 6; Length 456;
 Best Local Similarity 43.2%; Pred. No. 9,5e-10;
 Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRNGSLKRCXXKCSFXKAEIIFRNXXRTROFVSVY 44
 DB 43 ANSFLIEIRAGSLERECMEIEICDLEAQAEIFQNVDTLAIWISKY 86
 RESULT 6
 Q63207 PRELIMINARY; PRT; 482 AA.
 AC Q63207;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Factor X.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=96093366; PubMed=8578539;
 RA Stanton C., Ross R.P., Hutson S., Wallin R.,
 RT "Evidence for competition between vitamin K-dependent clotting factors
 RT for intracellular processing by the vitamin K-dependent gamma-
 RT carboxylase."
 RL Thromb. Res. 80:63-73(1995).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: X79807; CA56202.1; -.
 DR HSSP: P00742; 1XKA.
 DR MEROPS: S01.216; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.

```
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 02846783954A698 CRC64;
```

```
Query Match 50.0%; Score 95; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 5.5e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
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OY 1 ANGFLXLRNGSLRXCRXXLCSPFXAXEIPFNXXRTQFWVSY 44
Db 41 ANSPFEIRKGNLERECVEICSFEBAREVFEDNKTTEFMNKY 84
```

RESULT 7

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OS4740 PRELIMINARY; PRT; 481 AA.
ID OS4740
AC OS4740.
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR FA10.
OS Mus musculus (Mouse).
OC Plasmid plusscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=9845493; PubMed=9783672;
RA Heidemann H.H., Kontermann R.B.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
```

```
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KM Repeat; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E5F9D97AE CRC64;
```

```
Query Match 48.4%; Score 92; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
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```
OY 1 ANGFLXLRNGSLRXCRXXLCSPFXAXEIPFNXXRTQFWVSY 44
Db 41 ANSPFEIRKGNLERECVEICSYEVRERTEDEDKIKYWTKY 84
```

RESULT 8

```
O99L32 PRELIMINARY; PRT; 481 AA.
ID O99L32
AC O99L32.
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubeberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
```


DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 481 AA; 5400 MW; BD88B96C8A0B7E7F CRC64;
 Query Match 48.4%; Score 92; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 2e-08;
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANGFLLXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTROFVSY 44
 DB 41 ANSFPEEFKKNLERECMEICSEYEVEEIFEDEDKTEWTKY 84
 RESULT 9
 ID 088947 PRELIMINARY; PRT; 481 AA.
 AC 088947;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Coagulation factor X precursor.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
 RX MEDLINE=98347933; PubMed=9684791;
 RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
 RA Castellino F.J., Rosen E.D.;
 RT "Cloning and characterization of a cDNA encoding murine coagulation
 factor X.";
 RL Thromb. Haemost. 80:87-91(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvJ;
 RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
 RT "Cloning and characterization of the murine Factor X Gene.";
 RL Thromb. Haemost. 0:0-0(2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL; AF087644; AAC36345.1; -;
 DR HSSP; AF211347; AAF22980.1; -;
 DR HSSP; P00742; 1XKA.
 DR MEROPS; S01.216; -;
 DR MGD; MGI:103107; F10.
 DR InterPro; IPR000152; Asx_hydroxy1.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease; Signal.
 FT SIGNAL 1 40
 FT CHAIN 41 481
 SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9PD271E CRC64;
 Query Match 48.4%; Score 92; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 2e-08;
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANGFLLXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTROFVSY 44
 DB 41 ANSFPEEFKKNLERECMEICSEYEVEEIFEDEDKTEWTKY 84
 RESULT 10
 ID 095ME8 PRELIMINARY; PRT; 49 AA.
 AC 095ME8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Coagulation factor IX (Fragment).
 GN Bos taurus (Bovine).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mziara M.N., Amaral E.J.;
 RT "Partial sequence of bovine F9 coding gene."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB394598; AAK77556.1; -;
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR PROSITE; PS00011; GLUT CARBOXYLATION; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 49 49
 SQ SEQUENCE 49 AA; 6023 MW; D15C6D59CBA4A14 CRC64;
 Query Match 46.3%; Score 88; DB 6; Length 49;
 Best Local Similarity 37.2%; Pred. No. 1.1e-08;
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
 QY 2 NGFLXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTROFVSY 44
 DB 6 SGKLEEFVGNLERECMEICSEYEVEEIFEDEDKTEWTKY 48
 RESULT 11
 ID 014316 PRELIMINARY; PRT; 456 AA.
 AC 014316;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-AUG-1999 (TrEMBLrel. 11, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
 DE disease, HAEMOPHILIA B) (Factor IX).
 GN F9 OR FACTOR IX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bird C.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
  Brier E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
  TRYPSIN FAMILY.
CC EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_Ty.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
  Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 46.3%; Score 88; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLNGSLXRCXKXLCSPFXAEXIFRNXXRTQFWFSY 44
Db 44 SGKLEPVOGNLERCEMEKCSFEAREVFENTERTTFWKQY 86

RESULT 12
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
  chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.

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DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLNGSLXRCXKXLCSPFXAEXIFRNXXRTQFWFSY 44
Db 49 SGKLEPVOGNLERCEMEKCSFEAREVFENTERTTFWKQY 91

RESULT 13
O95ND6 PRELIMINARY; PRT; 461 AA.
AC O95ND6
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
  chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

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DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTQPFWSY 44
 Db 49 GGLLEEFVQGNLRECEMEKCSFEARAEVENTERTTEPFKQY 91

RESULT 14

O9GMD9 PRELIMINARY; PRT; 469 AA.

AC 09GMD9; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Coagulation factor X.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OX NCBI_Taxid=9258;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21015017; PubMed=11132153;
 RA Poorafshan M., Aveskog M., Munday B., Hellman L.;
 RT "Identification and structural analysis of four serine proteases in a
 RT monotreme, the platypus, Ornithorhynchus anatinus";
 RL Immunogenetics 52:19-28(2000).
 CC -! SIMILARITY. BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.

DR EMBL; AF275654; AAG00453.1; -.
 DR HSSP; P00742; 1XKB.
 DR MEROPS; S01.216; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GLA; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 46.3%; Score 88; DB 6; Length 469;
 Best Local Similarity 34.1%; Pred. No. 1.e-07;

Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTQPFWSY 44
 Db 41 ANSLFELKKGNIERECNETCSYEAREVFEEDTDKTNERWNIY 84

RESULT 15

O28994 PRELIMINARY; PRT; 138 AA.

AC O28994; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mature porcine factor IX (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96003866; PubMed=7568220;
 RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
 RT "X-ray structure of clotting factor IXa: active site and module
 RT structure related to Xase activity and hemophilia B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Lollar P.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U51135; AA96318.1; -.
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GLA; 1.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
 FT NON TER 1
 FT NON TER 138
 SQ SEQUENCE 138 AA; 15515 MW; 793BABDE4D5FAFAD CRC64;

Query Match 42.6%; Score 81; DB 6; Length 138;
 Best Local Similarity 41.2%; Pred. No. 6.1e-07;
 Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Oy 11 GSLRXCRXXLCSPFXAEXIFRNXXRTQPFWSY 44
 Db 4 GNLEFCEIEKCSFEAREVFEEDTDKTNERWNIY 37

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	124	65.3	44	3	US-08-955-636-26
4	122	64.2	44	3	US-08-955-636-30
5	122	64.2	44	3	US-08-955-636-30
6	122	64.2	406	1	US-08-293-778-24
7	122	64.2	406	1	US-08-293-778-24
8	122	64.2	406	1	US-08-955-471-5
9	122	64.2	406	5	PCT-US92-10242-5
10	122	64.2	444	1	US-08-475-845-2
11	122	64.2	444	2	US-08-327-690-2
12	122	64.2	444	2	US-08-660-289-2
13	122	64.2	444	2	US-08-537-807-2
14	122	64.2	444	2	US-08-871-003-2
15	122	64.2	444	3	US-08-464-233-2
16	122	64.2	444	4	US-08-189-607-2
17	122	64.2	444	4	US-09-378-907-2
18	122	64.2	444	5	PCT-US94-05779-2
19	122	64.2	466	1	US-07-882-202A-4
20	122	64.2	466	1	US-08-021-615A-4
21	122	64.2	466	4	US-08-321-777-4
22	122	64.2	466	4	US-09-009-217-14
23	122	64.2	466	4	US-09-009-656-14
24	122	64.2	466	5	PCT-US93-04493-4
25	119	62.6	44	3	US-08-955-636-28
26	118	62.1	44	3	US-08-955-636-29
27	108	56.8	41	1	US-08-229-280-4

28	100	52.6	139	1	US-08-330-978-2	Sequence 2, Appl
29	100	52.6	139	1	US-08-474-042-2	Sequence 2, Appl
30	100	52.6	139	1	US-08-484-558-2	Sequence 2, Appl
31	100	52.6	139	1	US-08-774-592-2	Sequence 2, Appl
32	100	52.6	437	1	US-08-487-037-2	Sequence 2, Appl
33	100	52.6	437	1	US-08-487-037-3	Sequence 3, Appl
34	100	52.6	488	1	US-08-487-037-1	Sequence 1, Appl
35	99	52.1	44	3	US-08-955-636-23	Sequence 23, Appl
36	96	50.5	44	3	US-08-955-636-2	Sequence 2, Appl
37	95	50.0	448	1	US-08-295-411-3	Sequence 3, Appl
38	95	50.0	448	2	US-08-955-471-3	Sequence 3, Appl
39	95	50.0	448	5	PCT-US92-10068-1	Sequence 1, Appl
40	95	50.0	448	5	PCT-US92-10242-3	Sequence 3, Appl
41	94	49.5	41	1	US-08-229-280-5	Sequence 5, Appl
42	94	49.5	42	2	US-08-745-254A-2	Sequence 2, Appl
43	94	49.5	44	3	US-08-955-636-1	Sequence 1, Appl
44	94	49.5	45	2	US-08-965-832-2	Sequence 2, Appl
45	94	49.5	419	1	US-08-295-411-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      81.6%; Score 155; DB 3; Length 44;
Best local Similarity 95.5%; Pred. No. 1.9e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCRX...XXAEXIFRNXXRTQFWVS 44
Db 1 ANGFLXLRNGSLXRCRX...XXAEXIFRNXXRTQFWVS 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match 65.8%; Score 125; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2.3e-14;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 ANGFLLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWISY 44
DB 1 ANAFLLXLRDGLXRXCKXQCSFXXARXIFPDAXRTKLFWISY 44

RESULT 3

US-08-955-636-26
Sequence 26, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 65.3%; Score 124; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGFLLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWISY 44
DB 1 ANAFLLXLRDGLXRXCKXQCSFXXARXIFPDAXRTKLFWISY 44

RESULT 4

US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match 64.2%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.3e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGFLLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWISY 44
DB 1 ANAFLLXLRDGLXRXCKXQCSFXXARXIFPDAXRTKLFWISY 44

RESULT 5
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 64.2%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.3e-14;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 ANGFLLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWISY 44
DB 1 ANAFLLXLRDGLXRXCKXQCSFXXARXIFPDAXRTKLFWISY 44

RESULT 6
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaissen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:

Query Match 64.2%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.3e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-293-778-24

Query Match      64.2%; Score 122; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPXXAEXIFRNXXRTROPFWSY 44
Db 1 ANAFLLYLRPGSLRYCKYQCSFYARIFYKDAERTKLFWISY 44

RESULT 7
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match      64.2%; Score 122; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPXXAEXIFRNXXRTROPFWSY 44
Db 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152

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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 64.2%; Score 122; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGLFLXLRNGSLKRXCRXXLCSEFXAXEIPFNXXRTQFWVSY 44
DB 1 ANAFLELRPGSLERCKEEOCSFEAREIFKDAERTYLFWISY 44

RESULT 9
PCT-US92-10242-5

Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Messers, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5
Query Match 64.2%; Score 122; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGLFLXLRNGSLKRXCRXXLCSEFXAXEIPFNXXRTQFWVSY 44
DB 1 ANAFLELRPGSLERCKEEOCSFEAREIFKDAERTYLFWISY 44

RESULT 10
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2
Query Match 64.2%; Score 122; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGLFLXLRNGSLKRXCRXXLCSEFXAXEIPFNXXRTQFWVSY 44
DB 39 ANAFLELRPGSLERCKEEOCSFEAREIFKDAERTYLFWISY 82
RESULT 11
US-08-327-690-2


```
/ Sequence 2, Application US/08327690
/ Patent No. 5817788
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Steuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-327-690-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/660,289
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/475,845
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: 08/327,690
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-660-289-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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QY 1 ANGFLXXLRNGSLKRCXXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 39 ANAFLELRPSLRECKEBCSFEAREIFKDAERTKLFMISY 82

RESULT 13
US-08-537-807-2
/ Sequence 2, Application US/08537807
/ Patent No. 5861374
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/537,807
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/05779
/ FILING DATE: 23-MAY-1994
/ APPLICATION NUMBER: US 08/065,725
/ FILING DATE: 21-MAY-1993
/ PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCRXCLCFXAXEIPFNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEKGCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 514
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCRXCLCFXAXEIPFNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEKGCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend, Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 64.2%; Score 122; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCRXCLCFXAXEIPFNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEKGCSFEAREIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:19
Job time : 10.75 secs

GenCode version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLLRNGSLRXCRXX.....XXAEXIFRNXXRRQFWVSX 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubppa/PCUS_PUBCOMB.pep.*
- 8: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	64.2	406	US-10-109-498-1	Sequence 1, Appli
2	94	49.5	419	US-10-182-263-1	Sequence 1, Appli
3	94	49.5	419	US-10-182-263-3	Sequence 3, Appli
4	94	49.5	419	US-10-182-263-4	Sequence 4, Appli
5	94	49.5	419	US-10-182-263-5	Sequence 5, Appli
6	94	49.5	419	US-09-978-917A-4	Sequence 2, Appli
7	94	49.5	461	US-10-182-263-2	Sequence 2, Appli
8	94	49.5	461	US-09-978-917A-2	Sequence 2, Appli
9	93	48.9	419	US-10-182-263-6	Sequence 6, Appli
10	88	46.3	415	US-09-118-748-2	Sequence 6, Appli
11	88	46.3	461	US-10-132-829-5	Sequence 5, Appli
12	88	46.3	461	US-09-884-901-3	Sequence 3, Appli
13	70	36.8	96	US-09-759-1308-313	Sequence 313, App
14	70	36.8	209	US-09-759-1308-312	Sequence 312, App
15	70	36.8	226	US-09-759-1308-310	Sequence 310, App
16	53	27.9	95	US-09-759-1308-356	Sequence 356, App
17	53	27.9	208	US-09-759-1308-355	Sequence 355, App
18	53	27.9	225	US-09-759-1308-353	Sequence 353, App
19	42	22.1	464	US-09-801-368-334	Sequence 334, App

20	41.5	21.8	197	9	US-10-076-622-516	Sequence 516, App
21	41.5	21.8	197	12	US-10-007-805-516	Sequence 516, App
22	41.5	21.8	232	9	US-10-076-622-517	Sequence 517, App
23	41.5	21.8	232	12	US-10-007-805-517	Sequence 517, App
24	41.5	21.8	243	9	US-09-938-418-7	Sequence 7, Appli
25	41.5	21.8	243	9	US-10-045-992-4	Sequence 4, Appli
26	41.5	21.8	243	9	US-10-063-547-122	Sequence 122, App
27	41.5	21.8	243	9	US-10-174-590-366	Sequence 366, App
28	41.5	21.8	243	9	US-10-176-758-366	Sequence 366, App
29	41.5	21.8	243	9	US-10-063-616-122	Sequence 122, App
30	41.5	21.8	243	9	US-10-175-737-366	Sequence 366, App
31	41.5	21.8	243	9	US-10-063-502-122	Sequence 122, App
32	41.5	21.8	243	9	US-10-076-622-514	Sequence 514, App
33	41.5	21.8	243	9	US-10-173-706-366	Sequence 366, App
34	41.5	21.8	243	9	US-10-175-738-366	Sequence 366, App
35	41.5	21.8	243	9	US-10-175-752-366	Sequence 366, App
36	41.5	21.8	243	9	US-10-176-482-366	Sequence 366, App
37	41.5	21.8	243	9	US-10-176-757-366	Sequence 366, App
38	41.5	21.8	243	9	US-10-176-913-366	Sequence 366, App
39	41.5	21.8	243	9	US-10-180-552-366	Sequence 366, App
40	41.5	21.8	243	9	US-10-180-557-366	Sequence 366, App
41	41.5	21.8	243	9	US-10-173-700-366	Sequence 366, App
42	41.5	21.8	243	9	US-10-174-572-366	Sequence 366, App
43	41.5	21.8	243	9	US-10-174-579-366	Sequence 366, App
44	41.5	21.8	243	9	US-10-174-582-366	Sequence 366, App
45	41.5	21.8	243	9	US-10-174-588-366	Sequence 366, App

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US2003004908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      64.2%; Score 122; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXLLRNGSLRXCRXXLCFXAXEYFRNXXRRQFWVSX 44
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Db 1 ANAFLLXLRPSLRLRXCKXXQCSFXARXIFKDXARXRLFWISY 44

RESULT 2
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXRCRXLCSPFXAEXIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXRCRXLCSPFXAEXIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFDVEDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXRCRXLCSPFXAEXIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXRCRXLCSPFXAEXIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 6
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 021998310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
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Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXE1FRNXXRTROFW 41
Db 1 ANSFLEELRHSSLERECIEICDFEEAKEIFQNVDDTLAFW 41

RESULT 7
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 49.5%; Score 94; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXE1FRNXXRTROFW 41
Db 43 ANSFLEELRHSSLERECIEICDFEEAKEIFQNVDDTLAFW 83

RESULT 8
US-09-978-917A-2
; Sequence 2, Application US/0978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 49.5%; Score 94; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXE1FRNXXRTROFW 41
Db 43 ANSFLEELRHSSLERECIEICDFEEAKEIFQNVDDTLAFW 83

RESULT 9

US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 48.9%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 3.1e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXE1FRNXXRTROFW 41
Db 1 ANSFLEELRHSSLERECIEICDFEEAKEIFQNVDDTLAFW 41

RESULT 10
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Staifford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 46.3%; Score 88; DB 10; Length 415;
Best Local Similarity 39.5%; Pred. No. 2.3e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRNGSLXRCXKXLCSEFXAXE1FRNXXRTROFW 44
Db 3 SKULBEFVQGNLRECEMEKCSFEFAREVENTERTTEFWKQY 45

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
; TITLE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-PA1170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query March          46.3%; Score 88; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY      2  NGFLXLRNGSLXRCRXKXLCSPFXAXEIRFNXXRTROPWVSY 44
Db      49  SGLKEEIVQGNLRECEMEKCSFEERAREVFENTERITTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query March          46.3%; Score 88; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY      2  NGFLXLRNGSLXRCRXKXLCSPFXAXEIRFNXXRTROPWVSY 44
Db      49  SGLKEEIVQGNLRECEMEKCSFEERAREVFENTERITTEFWKQY 91

RESULT 13
US-09-759-1308-313
; Sequence 313, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NM1M
; CURRENT APPLICATION NUMBER: US/09/759,1308
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-313

Query March          36.8%; Score 70; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 6.7e-05;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY      11  GSLXRCRXKXLCSPFXAXEIRFNXXRTROPWVSY 44
Db      46  GNLERECNEBLCNYEAREIFVDEBKXITAFWQVEY 79

RESULT 14
US-09-759-1308-312
; Sequence 312, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NM1M
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
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; PRIOR APPLICATION NUMBER: US 09/608,452
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/393,996
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 09/602,871
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 09/420,707
 ; PRIOR FILING DATE: 1999-10-19
 ; NUMBER OF SEQ ID NOS: 460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 312
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-759-130B-312

Query Match 36.8%; Score 70; DB 9; Length 209;
 Best Local Similarity 38.2%; Pred. No. 0.00015;
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXRCRXXLCSPXXAEXIFRNXXRTRQFWVS 44
 DB 46 GNLERCNEELCNVEEARLIFVDEDKTIAFWQEI 79

RESULT 15

; US-09-759-130B-310
 ; Sequence 310, Application US/09759130B
 ; Publication No. US20030022279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: McCarthy, Sean A
 ; APPLICANT: Fraser, Christopher C
 ; APPLICANT: Sharp, John D
 ; APPLICANT: Barnes, Thomas S
 ; APPLICANT: Kirtel, Susan J
 ; APPLICANT: Mackay, Charles R
 ; APPLICANT: Myers, Paul S
 ; APPLICANT: Leiby, Kevin R
 ; APPLICANT: Wrighton, Nicolas
 ; APPLICANT: Goodearl, Andrew
 ; APPLICANT: Holtzman, Douglas A
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
 ; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
 ; TITLE OF INVENTION: USES.
 ; FILE REFERENCE: MPIO0-535OMNIM
 ; CURRENT APPLICATION NUMBER: US/09/759,130B
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: US 09/479,249
 ; PRIOR FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: US 09/559,497
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/596,194
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/342,364
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: US 09/608,452
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/393,996
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 09/602,871
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 09/420,707
 ; PRIOR FILING DATE: 1999-10-19
 ; NUMBER OF SEQ ID NOS: 460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 310
 ; LENGTH: 226
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 ; US-09-759-130B-310

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 Best Local Similarity 38.2%; Pred. No. 0.00016;
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXRCRXXLCSPXXAEXIFRNXXRTRQFWVS 44
 DB 63 GNLERCNEELCNVEEARLIFVDEDKTIAFWQEI 96

Search completed: March 20, 2003, 13:30:17
 Job time : 9.375 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.101002.*

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	80.6	44	20	AA19306
2	154	80.6	44	22	AA18306
3	128	67.0	44	20	AA18312
4	122	63.9	44	20	AA18311
5	121	63.4	44	20	AA18310
6	119	62.3	44	20	AA18302
7	119	62.3	44	20	AA18305
8	119	62.3	44	22	AA18305
9	119	62.3	401	22	AA184870
10	119	62.3	401	22	AA184871

11	119	62.3	406	14	AA18306	Factor VII (VII).
12	119	62.3	406	18	AA18306	Modified blood coa
13	119	62.3	406	18	AA18306	Modified blood coa
14	119	62.3	406	22	AA18306	Human factor VIIa
15	119	62.3	406	22	AA18306	Human factor VIIa
16	119	62.3	406	22	AA18306	Human factor VIIa
17	119	62.3	406	22	AA18306	Human factor VIIa
18	119	62.3	406	22	AA18306	Human factor VIIa
19	119	62.3	406	22	AA18306	Human factor VIIa
20	119	62.3	406	22	AA18306	Human factor VIIa
21	119	62.3	406	22	AA18306	Human factor VIIa
22	119	62.3	406	22	AA18306	Human factor VIIa
23	119	62.3	406	22	AA18306	Human factor VIIa
24	119	62.3	406	22	AA18306	Human factor VIIa
25	119	62.3	406	22	AA18306	Human factor VIIa
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28	119	62.3	406	22	AA18306	Human factor VIIa
29	119	62.3	406	22	AA18306	Human factor VIIa
30	119	62.3	406	22	AA18306	Human factor VIIa
31	119	62.3	406	22	AA18306	Human factor VIIa
32	119	62.3	406	22	AA18306	Human factor VIIa
33	119	62.3	406	22	AA18306	Human factor VIIa
34	119	62.3	406	22	AA18306	Human factor VIIa
35	119	62.3	406	22	AA18306	Human factor VIIa
36	119	62.3	406	22	AA18306	Human factor VIIa
37	119	62.3	406	22	AA18306	Human factor VIIa
38	119	62.3	406	22	AA18306	Human factor VIIa
39	119	62.3	406	22	AA18306	Human factor VIIa
40	119	62.3	406	22	AA18306	Human factor VIIa
41	119	62.3	406	22	AA18306	Human factor VIIa
42	119	62.3	406	22	AA18306	Human factor VIIa
43	119	62.3	406	22	AA18306	Human factor VIIa
44	119	62.3	406	22	AA18306	Human factor VIIa
45	119	62.3	406	22	AA18306	Human factor VIIa

ALIGNMENTS

RESULT 1	
AA18306	
ID	AA18306 standard; peptide; 44 AA.
XX	
AC	AA18306;
XX	
DT	17-AUG-1999 (first entry)
DE	
XX	Bovine factor VII GLA domain.
DE	
XX	
KW	GLA domain; vitamin K-dependent protein; clotting disorder;
XX	therapy.
OS	Bos taurus.
XX	
FH	Key
FT	Misc-difference 1.44
FT	Location/Qualifiers
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	
PN	MO9920767-A1.
XX	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98WO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MINU) UNIV MINNESOTA.
XX	
PI	Nelaeuten GL;
XX	
DR	WPI; 1999-288309/24.

```

XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX PS Disclosure; Page 15; 86pp; English.
XX CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
SQ Sequence 44 AA;

Query Match 80.6%; Score 154; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.7e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRNGSLKRCXKXLCSPFXAXFIFRNXXRTQFWVSY 44
    |||||
Db 1 ANGFLXXLRPGSLKRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44

RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
AC AAB36396;
XX
XX 27-FEB-2001 (first entry)
XX
DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Bos taurus.
XX OS
XX WO20006753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Neiseetuen GL;
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot

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CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX Sequence 44 AA;
SQ

Query Match 80.6%; Score 154; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.7e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRNGSLKRCXKXLCSPFXAXFIFRNXXRTQFWVSY 44
    |||||
Db 1 ANGFLXXLRPGSLKRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44

RESULT 3
AAY18312
ID AAY18312 standard; peptide; 44 AA.
AC AAY18312;
XX
XX 17-AUG-1999 (first entry)
XX
XX Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc-difference 1..44 "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Neiseetuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;
SQ

Query Match 67.0%; Score 128; DB 20; Length 44;
Best Local Similarity 77.3%; Pred. No. 4e-14;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```

Qy 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAXFI FRNXXRTROPFWSY 44
 Db 1 ANAFLLXXLRPGSLXRXCKXXQCSFXAXFI FKDAAXRTKLFWISY 44

RESULT 4
 ID AAY18311 standard; peptide; 44 AA.

XX AAY18311;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN WO920767-A1.

XX 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsestuen GL;

XX WPI; 1999-288309/24.

XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain; useful for treating clotting disorders

PS Disclosure; Page 80; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

SQ Sequence 44 AA;

Query Match 63.9%; Score 122; DB 20; Length 44;

Best Local Similarity 75.0%; Pred. No. 4e-13; Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAXFI FRNXXRTROPFWSY 44
 Db 1 ANAFLLXXLRPGSLXRXCKXXQCSFXAXFI FKDAAXRTKLFWISY 44

RESULT 5
 ID AAY18310 standard; peptide; 44 AA.

XX AAY18310;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN WO920767-A1.

XX 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsestuen GL;

XX WPI; 1999-288309/24.

XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain; useful for treating clotting disorders

PS Disclosure; Page 80; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

SQ Sequence 44 AA;

Query Match 63.4%; Score 121; DB 20; Length 44;

Best Local Similarity 75.0%; Pred. No. 5.9e-13; Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAXFI FRNXXRTROPFWSY 44
 Db 1 ANAFLLXXLRPGSLXRXCKXXQCSFXAXFI FKDAAXRTKLFWISY 44

RESULT 6
 ID AAY18302 standard; peptide; 44 AA.

XX AAY18302;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"

PN WO9920767-A1.
 XX 29-APR-1999.
 XX
 XX 20-OCT-1998; 98WO-US22152.
 PF
 XX 23-OCT-1997; 97US-0955636.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA
 XX Nelsestuen GL;
 PI
 XX WPI; 1999-288309/24.
 DR
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Claim 11; Page 81; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX Sequence 44 AA;
 SQ
 Query Match 62.3%; Score 119; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRCXRLCSFXAPFIPRNXXRTQFWVS 44
 1 ANAFLXLRQSLXRCXRCXQCSFXAXRIFDAXRKLFWISY 44
 Db
 RESULT 7
 ID AAY18305 standard; peptide; 44 AA.
 XX
 AC AAY18305;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Human factor VII GLA domain.
 XX
 KW GLA domain; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 PD
 XX 20-OCT-1998; 98WO-US22152.
 PF
 XX 23-OCT-1997; 97US-0955636.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA
 XX Nelsestuen GL;
 PI
 XX WPI; 1999-288309/24.
 DR
 XX

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 XX Disclosure; Page 15; 86pp; English.
 PS
 XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX Sequence 44 AA;
 SQ
 Query Match 62.3%; Score 119; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRCXRLCSFXAPFIPRNXXRTQFWVS 44
 1 ANAFLXLRPGSLXRCXRCXQCSFXAXRIFDAXRKLFWISY 44
 Db
 RESULT 8
 ID AAB36395 standard; peptide; 44 AA.
 XX
 AC AAB36395;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Homo sapiens.
 XX
 XX WO20006753-A2.
 XX
 PD 09-NOV-2000.
 PD
 XX 28-APR-2000; 2000WO-US11416.
 PF
 XX 29-APR-1999; 99US-0302239.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA
 XX Nelsestuen GL;
 PI
 XX WPI; 2001-007226/01.
 DR
 XX
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 PS Disclosure; Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified

CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.

XX Sequence 44 AA;

Query Match 62.3%; Score 119; DB 22; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.1e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXRLCSFXAXFIRNXXRTQFWVS 44
 Db 1 ANAFLEELRPGSLERBECKECSFEARERIFKDAERTKLFWISY 44

RESULT 9
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.

XX AAB84870;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 mutant; mutcin.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 311..317

/note="Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19463.

XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 62.3%; Score 119; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXRLCSFXAXFIRNXXRTQFWVS 44
 Db 1 ANAFLEELRPGSLERBECKECSFEARERIFKDAERTKLFWISY 44

RESULT 10

AAB84871
 ID AAB84871 standard; Protein; 401 AA.

XX AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 mutant; mutcin.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 235..239

/note="Wild-type Val-Pro-Gly-Thr substituted by
 Asp-Arg-Lys-Thr-Leu"

/note="Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 62.3%; Score 119; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 1.1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXRLCSFXAXFIRNXXRTQFWVS 44
 Db 1 ANAFLEELRPGSLERBECKECSFEARERIFKDAERTKLFWISY 44

RESULT 11
 AAR35764
 ID AAR35764 standard; protein; 406 AA.

XX AAR35764;

DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

KM P.; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
 KM Factor VII; C; chymotrypsinogen; SP; serine protease; binding;
 KM exosite; catalytic activity.

OS Homo sapiens.
 OS XX

Key Location/Qualifiers
Region 1..152
/note= "Factor VII light chain"
Region 153..406
/note= "Factor VII heavy chain"
Peptide 374..388
/note= "exosite 1"
Peptide 290..310
/note= "exosite 2"
Peptide 290..310
/note= "pref. PC polypeptide; claim 2, page 136"
Peptide 374..388
/note= "pref. PC polypeptide; claim 2, page 136"
Peptide 289..304
/note= "pref. PC polypeptide; claim 4, page 137"
Peptide 290..304
/note= "pref. PC polypeptide; claim 4, page 137"
Peptide 245..266
/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
MO309804-A.
27-MAY-1993.
18-NOV-1992; 92WO-US10242.
18-NOV-1991; 91US-0793989.
(SCRI) SCRIPPS RES INST.
Griffin JH, Meesters RM;
WPI; 1993-182244/22.
Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
Disclosure; Page 133-135; 149pp; English.
The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm.
NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
Sequence 406 AA;
Query Match 62.3%; Score 119; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
1 ANGFLXLRNGSLXRXCRXLCSFXXAFIFNXXRTROFWVS 44
1 ANAFLELRPGSLERCKEQCSFEARRTIFDARTKLFWISY 44
RESULT 12
AAW14509
ID AAW14509 standard; protein; 406 AA.
XX AAW14509;
AC
XX
DT 14-MAY-1997 (first entry)
XX
DE Modified blood coagulation Factor VII (R290S).
XX
KW Blood coagulation; factor 7; mutein; mutation; modification;

thrombocytopenia; von Willebrand's disease; plasma substitute.
Homo sapiens.
Synthetic.
Key
Modified-site
Location/Qualifiers
6
/label= OTHER
/note= "gamma-carboxyglutamic acid"
7
/label= OTHER
/note= "gamma-carboxyglutamic acid"
14
/label= OTHER
/note= "gamma-carboxyglutamic acid"
16
/label= OTHER
/note= "gamma-carboxyglutamic acid"
19
/label= OTHER
/note= "gamma-carboxyglutamic acid"
20
/label= OTHER
/note= "gamma-carboxyglutamic acid"
25
/label= OTHER
/note= "gamma-carboxyglutamic acid"
26
/label= OTHER
/note= "gamma-carboxyglutamic acid"
29
/label= OTHER
/note= "gamma-carboxyglutamic acid"
32..33
/note= "gamma-carboxyglutamic acid"
35
/label= OTHER
/note= "gamma-carboxyglutamic acid"
38..39
/note= "gamma-carboxyglutamic acid"
42..43
/note= "proteolytic site"
44..45
/note= "proteolytic site"
50..61
/note= "proteolytic site"
55..70
/label= OTHER
/note= "beta-hydroxy-aspartic acid"
72..81
/note= "beta-hydroxy-aspartic acid"
91..102
/note= "beta-hydroxy-aspartic acid"
98..112
/note= "beta-hydroxy-aspartic acid"
114..127
/note= "beta-hydroxy-aspartic acid"
135..162
/note= "beta-hydroxy-aspartic acid"
143..144
/note= "proteolytic site"
145
/note= "proteolytic site"
159..164
/note= "proteolytic site"
178..194
/note= "proteolytic site"
193
/note= "proteolytic site"
242
/note= "proteolytic site"
244
/note= "proteolytic site"
290..291
/note= "proteolytic site in unmodified factor VII"
290
/note= "proteolytic site in unmodified factor VII"
310..329
/note= "proteolytic site in unmodified factor VII"
315..316
/note= "proteolytic site in unmodified factor VII"

FT Modified-site 322 /note= "glycosylation site"
 FT Disulfide-bond 340..368
 FT Cleavage-site 341..342
 FT Cleavage-site /note= "proteolytic site"
 FT Cleavage-site 392..393 /note= "proteolytic site"
 FT Cleavage-site 396..397 /note= "proteolytic site"
 FT Cleavage-site 402..403 /note= "proteolytic site"
 FT Cleavage-site /note= "proteolytic site"
 FT US5580560-A.
 PN 03-DEC-1996.
 XX 13-NOV-1989; 89US-0434149.
 PF 09-AUG-1993; 93US-0104509.
 PR 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0898248.
 PR 22-AUG-1994; 94US-0293778.
 XX (NOVO) NOVO-NORDISK AS.
 PA Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;
 PI WPI; 1997-033523/03.
 DR Mutated human factor VII or VIIa proteins - with amino acid
 XX substitutions to improve proteolytic stability
 PT Example 3; Page -: 28pp; English.
 XX Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys33, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.
 CC
 XX
 SQ Sequence 406 AA;
 QY 1 ANGELXXLRNGSLRXCRRXXLCSPFXAEXIFRNXXRTROFVWSY 44
 Db 1 ANAFLEBLRPGSLERCKEBCQCFEEAREIFKDAERTKLFWISY 44
 Query Match 62.3%; Score 119; DB 18; Length 406;
 Best local Similarity 52.3%; Pred. No. 1,1e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

FT Modified-site 6 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 7 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 14 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 16 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 19 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 20 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Disulfide-bond 17..22 /label= OTHER
 FT Modified-site 25 /note= "gamma-carboxyglutamic acid"
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 26 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 29 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 32..33 /note= "proteolytic site"
 FT Modified-site 35 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 38..39 /note= "proteolytic site"
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 42..43 /note= "proteolytic site"
 FT Cleavage-site 44..45 /note= "proteolytic site"
 FT Disulfide-bond 50..61 /label= OTHER
 FT Disulfide-bond 55..70 /note= "beta-hydroxy-aspartic acid"
 FT Modified-site 63 /label= OTHER
 FT Disulfide-bond 72..81 /note= "glycosylation site"
 FT Disulfide-bond 91..102 /note= "glycosylation site"
 FT Disulfide-bond 98..112 /note= "glycosylation site"
 FT Disulfide-bond 114..127 /note= "glycosylation site"
 FT Disulfide-bond 135..162 /note= "glycosylation site"
 FT Cleavage-site 143..144 /note= "glycosylation site"
 FT Modified-site 145 /note= "glycosylation site"
 FT Disulfide-bond 159..164 /note= "glycosylation site"
 FT Disulfide-bond 178..194 /note= "glycosylation site"
 FT Active-site 193 /note= "glycosylation site"
 FT Active-site 242 /note= "glycosylation site"
 FT Active-site 344 /note= "glycosylation site"
 FT Cleavage-site 290..291 /note= "glycosylation site"
 FT Disulfide-bond 310..329 /note= "glycosylation site"
 FT Cleavage-site 315..316 /note= "glycosylation site"
 FT Misc-difference 315 /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT Modified-site 322 /note= "glycosylation site"
 FT Disulfide-bond 340..368 /note= "glycosylation site"
 FT Cleavage-site 341..342 /note= "glycosylation site"
 FT Cleavage-site 392..393 /note= "glycosylation site"

```

FT FT Cleavage-site /note= "proteolytic site"
FT FT 396..397
FT FT /note= "proteolytic site"
FT FT Cleavage-site 402..403
FT FT /note= "proteolytic site"
XX PN USS580560-A.
XX PD 03-DEC-1996.
XX PF 13-NOV-1989; 89US-0434149.
XX XX
XX PR 09-AUG-1993; 93US-0104509.
XX PR 13-NOV-1989; 89US-0434149.
XX PR 12-JUN-1992; 92US-0898248.
XX PR 22-AUG-1994; 94US-0293778.
XX XX
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;
XX DR WPI; 1997-033523/03.
XX PT Mutated human factor VII or VIIa proteins - with amino acid
XX PT substitutions to improve proteolytic stability
XX PS Example 4; Page -; 28pp; English.
XX CC Modified human factor VII or VIIa proteins are stabilised against
XX CC proteolytic cleavage by substitution of one of the residues Lys32,
XX CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX CC Lys341 by an amino acid that provides a proteolytically more stable
XX CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX CC bleeding disorders such as thrombocytopenia and von Willebrand's
XX CC disease. They are also suitable for addition to plasma substitutes.
XX CC The present sequence is a specific example of a modified factor VII
XX CC protein.
XX SQ Sequence 406 AA;

Query Match 62.3%; Score 119; DB 19; Length 406;
Best Local Similarity 52.3%; Pred. No. 1.1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRLNGSLRXCRXXLCSPFXAIFRNXXRTROFWVS 44
DB 1 ANAFLELRPGSLRECKEKGCSFEAREIFKDAERTLFWISY 44

RESULT 14
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX AC AAU77745;
XX DT 05-JUN-2002 (first entry)
XX DE Human factor VIIa active site mutant.
XX XX
XX KW Factor VIIa; human; shock heat treatment; protein stability;
XX KW protein manufacture; protein conformation; mutant; muten.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FH 193
XX FT /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 242
XX FT /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 344
XX FT /note= "Member of the factor VIIa catalytic triad"

```

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FT FT Misc-difference 344
FT FT /label= Gly, Met, Thr
FT FT /note= "Preferably Ala. wild type Ser"
XX XX
XX PN WO200177141-A1.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-DK00234.
XX XX
XX PR 06-APR-2000; 2000DK-0000573.
XX PR 17-APR-2000; 2000US-197650P.
XX XX
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Mathiesen F;
XX XX
XX DR WPI; 2001-657162/75.
XX XX
XX FT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX FT involves a shock heat treatment -
XX PS Disclosure; Page -; 22pp; English.
XX CC The invention describes a method of stabilising a polypeptide involving
XX CC shock heat treatment of the polypeptide. The method is useful in a
XX CC pharmaceutical composition, in the industrial or large scale method of
XX CC manufacturing a polypeptide, also as a unit operation during preparation,
XX CC purification, recovery and/or formulation of polypeptides. The shock heat
XX CC treatment improves the protein stability without substantial loss of
XX CC biological activity. The method can be applied to change polypeptide
XX CC conformation in a very fast and non-invasive manner. The polypeptide
XX CC formed is stable. The method is also useful for decreasing the
XX CC association of the polypeptide. This sequence represents a modified
XX CC human factor VIIa protein, mutated at the catalytic site, described
XX CC in the invention.
XX CC Note: This sequence does not appear in the specification but has
XX CC been obtained using information given in the invention.
XX SQ Sequence 406 AA;

Query Match 62.3%; Score 119; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 1.1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRLNGSLRXCRXXLCSPFXAIFRNXXRTROFWVS 44
DB 1 ANAFLELRPGSLRECKEKGCSFEAREIFKDAERTLFWISY 44

RESULT 15
AAM52171
ID AAM52171 standard; Protein; 406 AA.
XX AC AAM52171;
XX DT 07-FEB-2002 (first entry)
XX DE Human FVII SEQ ID NO 1.
XX XX
XX KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX KW cardiac; hepatocytic; cerebroprotective; haemophilia; liver disease;
XX KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX OS Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
XX FH Misc-difference 6
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 7
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"

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FT Misc-difference 14
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 20
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 25
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 26
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52
 /note= "O-glycosylated"
 FT
 FT Modified-site 60
 /note= "O-glycosylated"
 FT
 FT Modified-site 145
 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 /note= "proteolytic cleavage site converting FVII zymogen
 to an activated form, comprising two chains
 linked by a single disulphide bridge"
 FT
 FT Modified-site 322
 /note= "N-glycosylated"
 FT
 FT
 PN W0200158935-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001; 2001WO-DK00094.
 XX
 XX
 PR 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX
 PA (MAXY-) MAXYGEN ABS.
 XX
 PI Andersen KV, Pedersen AH, Bornaes C;
 XX
 DR WPI: 2001-581807/65.
 DR N-PDB; AAI99982.
 XX
 XX
 PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 PS Claim 1; Page 81-83; 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration
 CC between injections.
 XX
 SQ Sequence 406 AA;
 Query Match 62.3%; Score 119; DB 22; Length 406;
 Best Local Similarity 75.0%; Pred. No. 1.1e-11;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLLXXLRNGSLXRXCRXXLCSPXXAFXIFRNXXRTRQFWXY 44
 DB 1 AAMFLXXLRPGLXRXCKXXQCSFXXRXIFKDAKXKLFWISY 44

Search completed: March 19, 2003, 14:51:16
 Job time : 31.4375 secs

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 / Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLLNGSLXRCRX.....XXAFXIFRXRXRPFWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

PIR 73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	77.0	407	1 KFB07	coagulation factor
2	127	66.5	443	2 I46932	coagulation factor
3	119	62.3	466	1 KFH07	coagulation factor
4	103	53.9	461	1 JX0210	protein C (activat
5	102	53.4	461	1 S18994	protein C (activat
6	93	48.7	456	1 KXBO	protein C (activat
7	92	48.2	482	1 EXRT	coagulation factor
8	92	48.2	488	1 EXHU	coagulation factor
9	90	47.1	461	1 KXHU	protein C (activat
10	87	45.5	492	1 EXBO	coagulation factor
11	86	45.0	622	1 TBHU	thrombin (EC 3.4.2
12	85	44.5	416	1 KFB0	coagulation factor
13	85	44.5	461	1 KFHU	coagulation factor
14	83	43.5	617	2 A10511	thrombin (EC 3.4.2
15	83	43.5	618	2 A35827	thrombin (EC 3.4.2
16	80	41.9	452	1 A30351	coagulation factor
17	80	41.9	459	2 J00419	coagulation factor
18	79	41.4	475	1 EXCH	coagulation factor
19	77	40.3	625	1 TBBO	thrombin (EC 3.4.2
20	72	37.7	642	2 S53433	plasma protein S p
21	68	35.6	675	1 KXBO	plasma protein S p
22	67	35.1	642	2 S53434	plasma protein S p
23	67	35.1	646	2 S38819	plasma protein S p
24	67	35.1	676	1 KXHU	plasma protein S p
25	65	34.0	675	1 KXRT	plasma protein S p
26	64	33.5	422	1 KXHU	plasma protein Z p
27	60	31.4	336	1 KXBO	plasma protein Z p
28	58	30.4	675	1 KXMS	plasma protein S p
29	56	29.3	678	2 B48089	growth arrest-spec

30	55	28.8	673	2 A48089	growth arrest-spec
31	53	27.7	674	2 I55476	growth potentialin
32	52	27.2	605	1 MWLEB	E1 protein - bovin
33	52	27.2	620	1 MWLEB2	E1 protein - bovin
34	49	25.7	1217	2 T21403	hypothetical prote
35	48	25.1	413	1 VHVNIH	nucleoprotein - in
36	46.5	24.3	594	2 D84859	probable MAP kinase
37	46.5	24.3	603	2 C96575	probable MAP kinase
38	45.5	23.8	576	2 G96763	probable MAP kinase
39	45	23.6	448	2 T18710	hypothetical prote
40	45	23.6	687	2 T08528	probable DNA topoi
41	43.5	22.8	105	2 S09766	hypothetical prote
42	43.5	22.8	304	2 AF2942	5-dehydro-4-deoxyg
43	43.5	22.8	304	2 D98340	5-dehydro-4-deoxyg
44	43.5	22.8	2133	2 T42763	coagulation factor
45	43	22.5	440	2 C83368	probable MRS trans

ALIGNMENTS

RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C/Accession: A31979; C02074

R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A/Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; PMID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <PK>

R/McMullen, B.A.; Fujikawa, K.; Kiesel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor

A/Reference number: A44556; PMID:89213999; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carboxylate

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F:1-44/Domains: Gla domain homology (fragment) <GLA>

F:50-81/Domains: BGF homology <EG1>

F:91-127/Domains: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domains: trypsin homology <TRY>

F:6-7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/I

F:52/Binding site: carboxylate (Ser) (covalent) #status experimental

F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 77.0%; Score 147; DB 1; Length 407;

Best Local Similarity 68.2%; Pred. No. 4,1e-18;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy      1  ANGFLXLRNGSLKRXCRXLCSPFXAXKIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  ANGFLLELLPGLSRECKEELCSFEAREHVFQSTERTKQFWVSY 44

RESULT 2
146932
Coagulation factor VII - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C/Accession: 146932
R/Brother: A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A/Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A/Reference number: 146932; MUID:93190306; PMID:8383365
A/Accession: 146932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-443 <BRO>
A/Cross-references: GB:S56300; NID:g266294; PID:g266295
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <Gla>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match
Query Match 66.5%; Score 127; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 1,6e-14;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy      1  ANGFLXLRNGSLKRXCRXLCSPFXAXKIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      40 ANSFLELRPGSLRECKEELCSFEAREHVFQSTERTKQFWVSY 83

RESULT 3
KFH07
Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C/Accession: A28322; A23819; A31186; B31186; S63524
R/O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.V.; Hagen, F.S.; Murt
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A/Reference number: A28322; MUID:87260948; PMID:3037537
A/Accession: A28322
A/Molecule type: DNA
A/Residues: 1-466 <OHA>
A/Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R/Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A/Title: Characterization of a cDNA coding for human factor VII.
A/Reference number: A23819; MUID:86205965; PMID:3486420
A/Accession: A23819
A/Molecule type: mRNA
A/Residues: 1-466 <HAG>
A/Cross-references: GB:M13232; NID:g182799; PIDN:AAA8040.1; PID:g182801
R/Thim, L.; Bioern, S.; Christensen, M.; Nicolaissen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A/Reference number: A90539; MUID:89088153; PMID:3264725
A/Accession: A31186
A/Molecule type: protein
A/Residues: 61-212 <THI>
A/Accession: B31186
A/Molecule type: protein
A/Residues: 213-466 <TH2>
R/Bioern, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A/Reference number: A40529; MUID:91250411; PMID:1904059
A/Contents: annotation; carbohydrate binding sites
R/Persson, E.; Petersen, L.C.

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Eur. J. Biochem. 234, 293-300, 1995
A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A/Reference number: S63524; MUID:96096752; PMID:8529655
A/Accession: S63524
A/Molecule type: protein
A/Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
A/Genetics:
A/Gene: GDB:F7
A/Cross-references: GDB:119897; OMIM:227500
A/Map position: 13q34-13q34
A/Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C/Function:
A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser
coagulation factor IX in the presence of calcium and tissue factor
A/Pathway: blood coagulation extrinsic pathway
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamu
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <Gla>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66-67;74,76,79,80,85,86,89,96/Modified site: gamma-carboxylglutamic acid (Glu) #status e
F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,4
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:122/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carboxylate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F:253,302,404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match
Query Match 62.3%; Score 119; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 4,4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1  ANGFLXLRNGSLKRXCRXLCSPFXAXKIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 ANAFLELRPGSLRECKEELCSFEAREHVFQDARTLFWVSY 104

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N/Alternate names: vitamin K-dependent serine proteinase
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JX0210
R/Tada, N.; Sato, M.; Tsujimura, A.; Iwabe, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A/Title: Isolation and characterization of a mouse protein C cDNA.
A/Reference number: JX0210; MUID:92316897; PMID:1618739
A/Accession: JX0210
A/Molecule type: mRNA
A/Residues: 1-461 <TRD>
A/Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
A/Experimental source: liver
A/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg
B.
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamu
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PC>
F:42-196/Domain: light chain #status predicted <PC1>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PC2>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:192-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

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F:212-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
 F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 53.9%; Score 103; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 3e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44
 Db 42 ANSFLEMRPGSLERECMEICDFEEAOEIFQVVEDTLAWIKY 85

RESULT 5
 S18994
 protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
 C:Accession: S18994; S24312
 R:Okatufj, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 submitted to the EMBL Data Library, February 1992
 A:Description: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S18994

A:Accession: S18994
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA>
 A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
 R:Okatufj, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992
 A:Title: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA>
 A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine protease

F:1-35/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-461/Product: protein C #status predicted <PRC>
 F:91-130/Domain: EGF homology <EG1>
 F:139-174/Domain: EGF homology <EG2>
 F:213-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-319,238-255,373-387,398-426/Disulfide bonds: #stat
 F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 53.4%; Score 102; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 4.6e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44
 Db 42 ANSFLEMRPGSLERECMEICDFEEAOEIFQVVEDTLAWIKY 85

RESULT 6
 KXBO
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoproteolysin IIA; plasma protein C
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A26250; A18385; A100928
 R:Hong, G.L.; Balagaje, R.M.; Macgillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100
 A:Accession: A26250
 A:Molecule type: mRNA
 A:Residues: 1-456 <LON>
 R:Fernlund, P.; Stenflo, J.
 J. Biol. Chem. 257, 12170-12179, 1982
 A:Title: Amino acid sequence of the light chain of bovine protein C.
 A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385
 A:Molecule type: protein
 A:Residues: 40-194 <FER>
 A:Note: 82-Lys was also found
 R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
 A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A:Reference number: A19316; MUID:83169769; PMID:6572939

A:Contents: annotation; revision to residue 110
 R:Stenflo, J.; Fernlund, P.
 J. Biol. Chem. 257, 12180-12190, 1982
 A:Title: Amino acid sequence of the heavy chain of bovine protein C.
 A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386
 A:Molecule type: protein
 A:Residues: 197-454, 'pv' <STB>
 R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
 J. Biol. Chem. 258, 5548-5553, 1983
 A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p
 A:Reference number: A37541; MUID:83213513; PMID:6304092

A:Contents: annotation; activation; calcium binding
 R:Johnson, A.E.; Esmon, N.L.; Lave, T.M.; Esmon, C.T.
 J. Biol. Chem. 258, 5554-5560, 1983
 A:Title: Structural changes required for activation of protein C are induced by Ca2+ bind
 A:Reference number: A37542; MUID:83213514; PMID:6406503

A:Contents: annotation; activation; calcium binding
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg
 s.
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c)
 bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stero

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;
 F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
 F:24-83/Domain: Gla domain homology <GLA>
 F:30-39/Domain: propeptide #status predicted <PRO>
 F:40-194/Product: protein C light chain #status experimental <LCH>
 F:98-128/Domain: EGF homology <EG1>

F:137-172/Domain: EGF homology <EG2>
 F:197-456/Product: protein C heavy chain #status experimental <HCH>
 F:197-210/Domain: activation peptide #status experimental <APT>
 F:211-440/Domain: trypsin homology <TRY>
 F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat
 F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:352,298,397/Active site: His, Asp, Ser #status predicted
 F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.7%; Score 93; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 1.8e-08;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44
 Db 40 ANSFLEBLRGVNERCESEVCEFEAREEIFQVETDTMAFWFSY 83

RESULT 7
 EXRT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
 C/Accession: S49075; J04670; PS0191; PS0190; 162745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra-
 A/Reference number: A58498; MUID:96093366; PMID:8578533
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; MUID:96194815; PMID:8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
 A/Experimental source: Cos-1 cell
 R/Enjyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
 A/Reference number: PS0190; MUID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: protein
 A/Residues: 41-58, 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: I46196; MUID:94222160; PMID:8168596
 A/Accession: 162745
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:G415309; PIDN:BA04756.1; PID:G455396
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of
 C/Superfamily: blood coagulation
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <AP1>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-460/Domain: trypsin homology <TRY>
 F:46, 47, 54, 56, 59, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 41
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:274, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match 48.2%; Score 92; DB 1; Length 482;
 Beet Local Similarity 36.4%; Pred. No. 2.8e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLXLRNGSLRXRCXFXLCSFXXAFIFNNXXRTROFWFSY 44
 41 ANSPFEIKGNLRECEVEICSFEDARVFEEDNEKTFEFMKY 84

RESULT 8

EXHU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N/Alternate names: Stuart factor
 C/Species: Homo sapiens (hmn)
 C/Date: 15-Nov-1994 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
 C/Accession: A24478; J00917; A24485; A25853; A22208; A21284; A20362; S39415; I54051; A001
 R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A/Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e
 A/Reference number: A24478; MUID:87026600; PMID:3768336
 A/Accession: A24478
 A/Molecule type: DNA
 A/Residues: 1-488 <LEY>
 A/Cross-references: GB:L29433; GB:M14327; NID:G459809; PIDN:AAA52764.1; PID:G182831
 R/Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagu
 A/Reference number: J00917; MUID:91216473; PMID:1902434
 A/Accession: J00917
 A/Molecule type: mRNA
 A/Residues: 1-488 <MES>
 A/Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390
 R/Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagula
 A/Reference number: A42485; MUID:92218390; PMID:1313796
 A/Accession: A42485
 A/Molecule type: DNA
 A/Residues: 1-15 <MIA>
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:P:93787)
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A/Reference number: A25853; MUID:86221713; PMID:3011603
 A/Accession: A25853
 A/Molecule type: mRNA
 A/Residues: 19-284, 'E', 289-488 <KAU>
 A/Cross-references: GB:M22613; NID:G180335; PIDN:AAA51984.1; PID:G180336
 R/Fung, M.R.; Hay, C.W.; Macgillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A/Title: Characterization of an almost full-length cDNA coding for human blood coagulat
 A/Reference number: A22208; MUID:85216545; PMID:2582420
 A/Accession: A22208
 A/Molecule type: mRNA
 A/Residues: 13-441, 'S', 443-488 <FUN>
 A/Cross-references: GB:K03194; NID:G182840; PIDN:AAA52490.1; PID:G182841
 R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A/Title: Characterization of a cDNA coding for human factor X.
 A/Reference number: A21284; MUID:84222026; PMID:6587384
 A/Accession: A21284
 A/Molecule type: mRNA
 A/Residues: 13-284, 'E', 289-488 <LE2>
 A/Cross-references: GB:K01896
 R/McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Saegawa, T.; Howald, W.N.; Kwa, E.Y.; Weinstein
 Biochemistry 22, 2875-2884, 1983
 A/Title: Complete amino acid sequence of the light chain of human blood coagulation fact
 A/Reference number: A20362; MUID:83257207; PMID:6871167
 A/Accession: A20362
 A/Molecule type: protein
 A/Residues: 41-179 <CMC>
 R/Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39415
 A/Molecule type: protein
 A/Residues: 183-234 <INO>
 A/Note: glycosylation sites
 A/Note: identification and characterization of beta-hydroxyaspartic acid
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.

Gene 84, 517-519, 1989
 A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: I54051; MUID:90128229; PMID:2612918
 A:Accession: I54051
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:918360; PIDN:AA52636.1; PID:9553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Biol
 J. Mol. Biol. 222, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277; PMID:8355279
 A:Accession: A49458
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetics:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A>Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:91-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <APT>
 F:235-462/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 48.2%; Score 92; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 2.9e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLKRXCRXXLCSPXAFXIFRNXXRTROFVSY 44
 DB 41 ANSFLEEMKXGHLERECMEETCSYEAREVEDSDKTNEFNKY 84

RESULT 9

KXHU
 protein C (activated) (BC 3.4.21.69) precursor - human
 N:Alternate names: autoprotechombin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 A:Accession: A22331; A25426; A21781; A23789; A00927
 R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A>Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M1228; NID:9190333; PIDN:AAA60166.1; PID:9190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A>Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, 'L', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
 R:Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'Q', 107-461 <FOS2>
 A:Cross-references: GB:K02059; NID:9190322; PIDN:AAA60164.1; PID:9190323
 R:Beckmann, R.J.; Schmidt, R.J.; Sautter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and it
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
 R:Wietlich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
 A:Reference number: A44605; MUID:90293094; PMID:1694179
 A:Accession: A44605
 A:Contents: annotation; carboxylate binding sites; activation peptide
 A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544894
 A:Accession: A44606
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fi
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 A:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status experimental <APT>
 F:200-211/Domain: activation peptide #status experimental <ACT>
 F:212-445/Domain: trypsin homology <TRY>
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status expe
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carboxylate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (chrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 47.1%; Score 90; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 6.2e-08;
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLKRXCRXXLCSPXAFXIFRNXXRTROFV 41
 DB 43 ANSFLEEMKXGHLERECIBRICDFEAKETFOVNDTLATW 83

RESULT 10

EXBO
 coagulation factor Xa (BC 3.4.21.6) precursor - bovine

N/Alternate names: Stuart factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 C/Pung, M.R.; Campbell, R.M.; Macgillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A/Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A/Reference number: A22867; MUID:84247315; PMID:6330671
 A/Accession: A22867
 A/Molecule type: mRNA
 A/Residues: 1-487 <FNU>
 A/Cross-references: GB:X00673; NID:9192; PIDN:CAA25286.1; PID:9193
 R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A/Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A/Reference number: A14997; MUID:80130563; PMID:6766735
 A/Accession: A14997
 A/Molecule type: protein
 A/Residues: 41-102, 'N', 104-180 <ENF>
 R/McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Contents: annotation; revision to residue 103
 R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A/Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A/Reference number: A12030; MUID:76053069; PMID:1059093
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-282,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GRKG', 446-492 <I
 A/Note: carboxylate binding sites and disulfide bonds were determined
 R/Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A/Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A/Reference number: A34412; MUID:89380326; PMID:2789221
 A/Accession: A34412
 A/Molecule type: protein
 A/Residues: 85-128 <PER>
 A/Note: beta-hydroxyaspartic acid site
 R/Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39414
 A/Molecule type: protein
 A/Residues: 183-196,199-209,216-233 <INO>
 A/Note: carboxylate binding sites
 R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A/Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
 A/Reference number: A12453; MUID:70553314; PMID:4264286
 A/Contents: annotation; active site
 R/Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A/Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
 A/Reference number: A13504; MUID:76053121; PMID:1059122
 A/Contents: annotation; activation
 R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A/Reference number: A38024; MUID:84185716; PMID:6546930
 A/Contents: annotation; calcium binding
 R/Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A/Reference number: A38025; MUID:86140210; PMID:3949800
 A/Contents: annotation; sulfate binding
 C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C/Genetics:
 A/Gene: F10
 A/Map position: 13q34
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:41-180/Domain: Gla domain homology <Gla>
 F:90-122/Domain: coagulation factor X light chain #status experimental <LCH>
 F:90-122/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-233/Domain: activation peptide #status experimental <AP>
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F:234-461/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:209/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #statu
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
 F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 45.5%; Score 87; DB 1; Length 492;
 Best Local Similarity 36.4%; Pred. No. 2,2e-07;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLKRXCRXXLCSEFXAFPIRNXRTGQFVSVY 44
 Db 41 ANSFLEVKQNLRECELBACSLSEAREVPEDEAQTDFPSKY 84

RESULT 11
 TBHU
 thrombin (BC 3.4.21.5) precursor [validated] - human
 N/Alternate names: coagulation factor II
 N/Contents: prothrombin
 C/Species: Homo sapiens (man)
 C/Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
 C/Accession: A29351; A00914; B00914; A37549; A37550; I51952
 R/Degen, S.J.F.; Davie, E.W.
 Biochemistry 26, 6165-6177, 1987
 A/Title: Nucleotide sequence of the gene for human prothrombin.
 A/Reference number: A29351; MUID:88077877; PMID:2825773
 A/Accession: A29351
 A/Molecule type: DNA
 A/Residues: 1-622 <DEG>
 A/Cross-references: GB:M17262; GB:M363691; NID:9558069; PIDN:MAC63054.1; PID:9339641
 R/Degen, S.J.F.; Macgillivray, R.T.A.; Davie, E.W.
 Biochemistry 22, 2087-2097, 1983
 A/Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
 A/Reference number: A00914; MUID:83231469; PMID:6305407
 A/Accession: A00914
 A/Molecule type: mRNA
 A/Residues: 8-163, 'N', 165-622 <DE2>
 A/Cross-references: GB:V00585; GB:J00307; NID:937128; PIDN:CAA23842.1; PID:91335344
 A/Accession: B00914
 A/Molecule type: DNA
 A/Residues: 188-311 <DE3>
 R/Walz, D.A.; Hewett-Emlert, D.; Seegers, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1968-1972, 1977
 A/Reference number: A37549; MUID:77193964; PMID:266717
 A/Accession: A37549
 A/Molecule type: protein
 A/Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'WV', 196-308, '
 R/Burkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
 J. Biol. Chem. 255, 4942-4957, 1977
 A/Title: Primary structure of human prothrombin 2 and alpha-thrombin.

A/Reference number: A37550; PMID:77207112; PMID:873923
 A/Accession: A37550
 A/Molecule type: protein
 A/Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 R/Rabbit, M.J.; Blashill, A.; Furie, B.; Furie, B.C.
 J. Biol. Chem. 261, 13210-13215, 1986
 A/Reference number: A37551; PMID:87008532; PMID:3759958
 A/Contents: annotation; activation cleavages
 R/MacGillivray, R.T.; Irwin, D.M.; Guinco, E.R.; Stone, J.C.
 Ann. N.Y. Acad. Sci. 485, 73-79, 1986
 A/Title: Recombinant genetic approaches to functional mapping of thrombin.
 A/Reference number: I51952; PMID:87182874; PMID:3471151
 A/Accession: I51952
 A/Molecule type: mRNA
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 1-2, 'R', 5-100 <RES>
 A/Cross-references: GB:M3031; NID:q190723; PIND:AAA60220.1; PID:q190724
 C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
 C/Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
 C/Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain
 ter 314-Arg, are released in natural blood clotting.
 C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
 C/Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
 ent interaction with the negatively charged phospholipid membrane surface.
 C/Comment: The prothrombin precursor is synthesized in the liver.
 C/Genetics:
 A/Gene: GDB:F2
 A/Cross-references: GDB:119894; OMIM:176930
 A/Map position: 11p11-11q12
 A/Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 493/2; 491/2; 552
 C/Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C/Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
 F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-43/Domain: signal sequence #status predicted <PRO>
 F.28-87/Domain: Gla domain homology <Gla>
 F.144-322/Domain: prothrombin peptide #status experimental <MAT>
 F.144-327/Domain: activation peptide #status experimental <APT>
 F.108-186/Domain: kringle homology <KR2>
 F.213-291/Domain: kringle homology <KR2>
 F.328-363/Domain: thrombin light chain #status experimental <LCH>
 F.364-622/Domain: thrombin heavy chain #status experimental <HCH>
 F.364-613/Domain: trypsin homology <TRY>
 F.39-50, 57, 59, 62, 63, 68, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F.60-55, 90-103, 108-186, 129-169, 157-181, 213-291, 234-274, 262-286/Disulfide bonds: #status
 F.121, 143/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.336-482, 536-550, 564-594/Disulfide bonds: #status predicted
 F.391-407/Disulfide bonds: #status experimental
 F.406, 462/Active site: His, Asp #status predicted
 F.416/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.568/Active site: Ser #status experimental

Query Match 45.0%; Score 86; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred. No. 4.2e-07;
 Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANGEFLXLRNGSLXRCXXLCSPFXAFLFRNXXRRQFWVS 44
 Db 44 ANTFLEVRKGNLRECVETCTSEFAFEALSTADIVFAKY 87

RESULT 12
 KPEO
 coagulation factor IXa (BC 3.4.21.22) precursor - bovine
 N/Alternate names: Christmas factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text_change 16-Jul-1999
 C/Accession: A14757; B20274; I45891; A00923
 R/Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neuwath, H.; Davie, E.W.; Ti
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
 A/Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
 A/Reference number: A14757; PMID:80056619; PMID:291916
 A/Accession: A14757
 A/Molecule type: protein

A/Residues: 1-63, 'T', 65-416 <MAT>
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe
 A/Reference number: A20274; PMID:83308813; PMID:6688526
 A/Accession: B20274
 A/Molecule type: protein
 A/Residues: 59-63, 'X', 65-69 <MCW>
 A/Rhoad, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A/Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
 A/Reference number: I45891; PMID:82272386; PMID:6287289
 A/Accession: I45891
 A/Molecule type: mRNA
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 52-139 <CHO>
 A/Cross-references: GB:U00007; NID:q163053; PIND:AAA0520.1; PID:q163054
 R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
 J. Biochem. 104, 867-868, 1988
 A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A/Reference number: A44556; PMID:89213999; PMID:3149637
 A/Contents: annotation
 A/Note: structure and location of a carbohydrate covalently bound to Ser
 C/Comment: Factor IX is activated by factor Xa, which excises the activation peptide pr
 C/Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C/Function:
 A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser
 A/Pathway: blood coagulation intrinsic pathway
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
 F.1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
 F.1-45/Domain: Gla domain homology (fragment) <Gla>
 F.51-82/Domain: EGF homology <EG1>
 F.88-124/Domain: EGF homology <EG2>
 F.147-181/Domain: activation peptide #status experimental <APT>
 F.182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F.182-409/Domain: trypsin homology <TRY>
 F.7.8, 15, 17, 20, 21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F.18-23, 51-62, 56-71, 73-82, 88-99, 95-109, 111-124, 123-220, 207-223, 337-351, 362-390/Disulfide
 F.53/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F.54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F.158, 168, 177, 261/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.222, 270, 366/Active site: His, Asp, Ser #status predicted

Query Match 44.5%; Score 85; DB 1; Length 416;
 Best Local Similarity 37.2%; Pred. No. 4.3e-07;
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRNGSLXRCXXLCSPFXAFLFRNXXRRQFWVS 44
 Db 3 SGKLEFRVGNLRECKEKCSEAEAREVENTKTEFWKY 45

RESULT 13
 KPEO
 coagulation factor IXa (BC 3.4.21.22) precursor [validated] - human
 N/Alternate names: antihemophilic factor B; Christmas factor
 C/Species: Homo sapiens (man)
 C/Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text_change 15-Sep-2000
 C/Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20;
 R/Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A/Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A/Reference number: A00922; PMID:86000558; PMID:2994716
 A/Accession: A00922
 A/Molecule type: DNA
 A/Residues: 1-461 <YOS>
 A/Cross-references: GB:K02402; NID:q182612; PIND:AA85620.1; PID:q182613
 R/Johnson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro
 EMBO J. 3, 1053-1060, 1984
 A/Title: The gene structure of human anti-haemophilic factor IX.
 A/Reference number: A37570; PMID:84236100; PMID:6329734

A:Accession: A37570
 A:Molecule type: DNA
 A:Residues: 1-461 <ANS>
 A:Cross-references: GB:K02048
 R:Reitema, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A:Reference number: A30511; MUID:88327116; PMID:3416065
 A:Accession: A30511
 A:Molecule type: DNA
 A:Residues: 8-24 <RE>
 A:Cross-references: EMBL:X55008; NID:G311288; PIDN:CA838245.2; PID:G4469253
 R:Koebel, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A:Reference number: A32989; MUID:89371752; PMID:2739373
 A:Accession: A32989
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-92 <KOE>
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
 A:Reference number: A22673; MUID:85190593; PMID:3857619
 A:Accession: A22673
 A:Molecule type: mRNA
 A:Residues: 1-193; 'T', 195-461 <MCG>
 A:Cross-references: GB:M11309; NID:G180552; PIDN:AA52023.1; PID:G180553
 A:Note: the authors translated the codon ACA for residue 29 as Tyr
 R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohl, V.; Findel, A.; Tolero
 Nucleic Acids Res. 11, 2325-2335, 1983
 A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
 A:Reference number: A37546; MUID:84300526; PMID:6089357
 A:Accession: A37546
 A:Molecule type: Protein
 A:Residues: 38-193; 'T', 195-326 <JAG>
 A:Cross-references: GB:M35672
 R:Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A:Title: Isolation and characterization of a cDNA coding for human factor IX.
 A:Reference number: A30623; MUID:83065193; PMID:6959130
 A:Accession: A30623
 A:Molecule type: mRNA
 A:Residues: 1-12; 'S', 14-73; 'P', 75-82; 'K', 84-203; 'P', 205-216; 'G', 218-298; 'A', 299-356; 'A',
 A:Cross-references: GB:U00136; NID:G182608; PIDN:AA98726.1; PID:G182609
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A:Title: Development of an immunofluorescence process for factor IX purification.
 A:Reference number: A60486; MUID:90194857; PMID:2316207
 A:Accession: A60486
 A:Molecule type: Protein
 A:Residues: 47-52; 'XX', 55-60; 'X', 62; 'XX', 65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: Protein
 A:Residues: 105-109; 'X', 111-115 <MCM>
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A:Title: Characterisation of two differently processed forms of human recombinant factor
 A:Reference number: S02527; MUID:88166735; PMID:3280312
 A:Accession: S02527

A:Molecule type: Protein
 A:Residues: 23-63 <BAL>
 A:Note: processed forms expressed in recombinant system
 R:Julien, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Neulien, I
 EMBO J. 9, 3295-3301, 1990
 A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and
 A:Reference number: S12058; MUID:91006024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Baron, M.; Mayhew, M.; Willie, A.; Beeley, T.; Brownlee, G.G.; Campe
 EMBO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; MUID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: Protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charanlier, J.L.; Baes, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: S19612; MUID:94054330; PMID:8236150
 A:Accession: S19612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:G439773; PIDN:AA28588.1; PID:G439774
 R:Scoffet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: S19529; MUID:88127096; PMID:3340835
 A:Accession: S19529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M19063; NID:G182622; PIDN:AA52456.1; PID:G182623
 R:Abarwa, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically link
 A:Reference number: A54255; MUID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: Protein
 A:Residues: D', 204; 'X', 206-211; 212; 'D', 214; 'X', 216-221; 'D' <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Mortle, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5696-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Mortle, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding, correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation c
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Shinto, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX (B9) Nsgova: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078225; PMID:2592373

A;Contents: annotation; sequence of mutant B(M) Nagoya
 A;Note: carboxylation, glycosylation, and cleavage sites
 R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownie
 submitted to the Brookhaven Protein Data Bank, November 1991
 A;Reference number: A51252; PDB:1IXA
 A;Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A;Note: recombinant form expressed in yeast
 C;Comment: Factor IX is activated by factor Xla, which excises the activation peptide p
 C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C;Genetics:
 A;Gene: GDB:F9
 A;Cross-references: GDB:119900; OMIM:306900
 A;Map position: Xq27.1-Xq27.2
 A;Functions: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C;Function:
 A;Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 A;Pathway: blood coagulation intrinsic pathway
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
 F;1-28/Domain: signal sequence #status predicted <SIG>
 F;29-46/Domain: propeptide #status experimental <PRO>
 F;31-91/Domain: Gla domain homology <Gla>
 F;47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F;97-128/Domain: EGF homology <EGF>
 F;134-170/Domain: EGF homology <EG2>
 F;192-226/Domain: activation peptide #status experimental <ACT>
 F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F;227-454/Domain: trypsin homology <TRY>
 F;53,54,61,63,66,67,72,73,76,79,82,88/Modified site: gamma-carboxyglutamic acid (Glu) #
 F;64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F;99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F;191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
 F;203,213/Cleavage site: carboxylate (Asn) (covalent) #status experimental
 F;205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F;226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 44.5%; Score 85; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 4.8e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSPFXAFIFRNXXRTQFWVSY 44
 Db 49 SGLEEFVQGLRECEMEKCSFEAREVFNTERITTEFMKQY 91

RESULT 14
 S10511
 thrombin (EC 3.4.21.5) precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-May-1993 #sequence, revision 07-May-1993 #text_change 03-May-2002
 C;Accession: S10511; A60576; B42696
 R;Dhanich, M.; Monard, D.
 Nucleic Acids Res. 18, 4251, 1990
 A;Title: cDNA sequence of rat prothrombin.
 A;Reference number: S10511; MUID:90332426; PMID:2377469
 A;Accession: S10511
 A;Molecule type: mRNA
 A;Residues: 1-617 <DTH>
 A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
 R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
 Endocrinology 126, 167-175, 1990
 A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
 A;Reference number: A60576; MUID:90091942; PMID:2293980
 A;Accession: A60576
 A;Molecule type: protein
 A;Residues: 44-58 <HEN>
 A;Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
 R;Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A;Reference number: A42696; MUID:92212913; PMID:1557383

A;Accession: B42696
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 383-617, 'E', <BAN>
 A;Cross-references: GB:M81397
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-43/Domain: propeptide #status predicted <PRO>
 F;28-88/Domain: Gla domain homology <Gla>
 F;44-617/Product: prothrombin #status experimental <PMAT>
 F;109-187/Domain: kringle homology <KR1>
 F;215-292/Domain: kringle homology <KR2>
 F;360-609/Domain: trypsin homology <TRY>
 F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
 F;402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 43.5%; Score 83; DB 2; Length 617;
 Best Local Similarity 39.5%; Pred. No. 1.4e-06;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSPFXAFIFRNXXRTQFWVSY 44
 Db 46 SGLEELRKGNLRECEVCEQSYEAFALESQDITDFVAKY 88

RESULT 15
 A35827
 thrombin (EC 3.4.21.5) precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 14-Dec-1990 #sequence, revision 14-Dec-1990 #text_change 03-May-2002
 C;Accession: A35827; A42696; G12081
 R;Dege, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.;
 DNA Cell Biol. 9, 487-498, 1990
 A;Title: Characterization of the cDNA coding for mouse prothrombin and localization of t
 A;Reference number: A35827; MUID:91025551; PMID:2222810
 A;Accession: A35827
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-618 <DEG>
 A;Cross-references: GB:X52308; NID:953813; PIDN:CAA36548.1; PID:953814
 A;Experimental source: strain C57BL/6
 A;Note: the data were obtained from females resulting from the cross of M. domesticus and
 R;Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A;Reference number: A42696; MUID:92212913; PMID:1557383
 A;Accession: A42696
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 384-618, 'E', <BAN>
 A;Cross-references: GB:M81394
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
 F;1-24/Domain: signal sequence #status predicted <PRO>
 F;25-43/Domain: propeptide #status predicted <PRO>
 F;28-88/Domain: Gla domain homology <Gla>
 F;44-618/Product: prothrombin B #status predicted <MAT>
 F;109-187/Domain: kringle homology <KR1>
 F;215-293/Domain: kringle homology <KR2>
 F;361-610/Domain: trypsin homology <TRY>
 F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F;61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
 F;403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 43.5%; Score 83; DB 2; Length 618;
 Best Local Similarity 39.5%; Pred. No. 1.4e-06;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSPFXAFIFRNXXRTQFWVSY 44
 Db 46 SGLEELRKGNLRECEVCEQSYEAFALESQDITDFVAKY 88

Search completed: March 19, 2003, 15:01:02
Job time : 30.125 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLLNGSLXRCRX...XXAFXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	77.0	407	FA7_BOVIN	P22457 Bos taurus
2	127	66.5	444	FA7_RABIT	P8139 cyctolagus
3	119	62.3	466	FA7_HUMAN	P08709 homo sapien
4	105	55.0	218	TMG1_HUMAN	O14668 homo sapien
5	103	53.9	461	PRTC_MOUSE	P33587 mus musculu
6	102	53.4	446	FA7_MOUSE	P70375 mus musculu
7	98	51.3	231	TMG3_HUMAN	Q91227 mus musculu
8	98	51.3	459	PRTC_PIG	O91227 mus musculu
9	96	50.3	490	FA10_RABIT	O19045 cyctolagus
10	93	48.7	456	PRTC_BOVIN	P00745 Bos taurus
11	92	48.2	488	FA10_HUMAN	P00742 homo sapien
12	90	47.1	461	PRTC_HUMAN	P04070 homo sapien
13	87	45.5	492	FA10_BOVIN	P00723 Bos taurus
14	87	45.5	492	FA10_BOVIN	P00723 Bos taurus
15	86	45.0	622	THRB_HUMAN	P00724 Bos taurus
16	85	44.5	416	FA9_BOVIN	P00740 homo sapien
17	85	44.5	461	FA9_HUMAN	P25135 gallus galli
18	83	43.5	617	THRB_RAT	P18292 ratu
19	83	43.5	618	THRB_MOUSE	P19221 mus musculu
20	81	42.4	458	PRTC_RABIT	Q28661 cyctolagus
21	80	41.9	452	FA9_CANFA	P19540 canis fami
22	80	41.9	459	FA9_MOUSE	P16299 mus musculu
23	79	41.4	475	FA10_CHICK	P25135 gallus galli
24	77	40.3	625	THRB_BOVIN	P07224 Bos taurus
25	68	35.6	675	PRTC_BOVIN	O14668 homo sapien
26	67	35.1	202	TMG2_HUMAN	P08726 homo sapien
27	67	35.1	226	TMG4_HUMAN	P98110 cyctolagus
28	67	35.1	646	PRTC_RABIT	Q28520 macaca mula
29	67	35.1	649	PRTC_MACMU	P07223 Bos taurus
30	67	35.1	676	PRTC_HUMAN	P81428 tropidichis
31	65	34.0	376	FA10_TROCA	P53813 ratu
32	65	34.0	675	PRTC_RAT	P22891 homo sapien
33	64	33.5	400	PRTC_HUMAN	P22891 homo sapien

34	60	31.4	396	1	PRTC_BOVIN	P00744 Bos taurus
35	58	30.4	675	1	PRTC_MOUSE	Q08761 mus musculu
36	52	27.2	604	1	VE1_BPV2	P1298 bovine pap
37	52	27.2	605	1	VE1_BPV1	P03116 bovine pap
38	48	25.1	413	1	NCAP_HINV	P19691 infectious
39	45	23.6	818	1	CDB1_HUMAN	Q9553 homo sapien
40	43.5	22.8	105	1	UL03_HCMVA	P16775 human cyto
41	43.5	22.8	2133	1	FA8_PIG	P1263 sus scrofa
42	43	22.5	350	1	VOD1_DROME	Q9w4p5 drosophila
43	42	22.0	320	1	GSHB_BUCAL	P57612 buchne
44	42	22.0	473	1	FP2_MYGA	Q25464 mytilus gal
45	42	22.0	1275	1	RFBC_MYXXA	Q50864 myxococcus

ALIGNMENTS

RESULT 1	FA7_BOVIN	STANDARD;	PRT;	407 AA.
ID	FA7_BOVIN			
AC	P22457;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII (BC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89008362; PubMed=3049594;			
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,			
RA	Iwanaga S.;			
RT	"Bovine factor VII. Its purification and complete amino acid			
RT	sequence.";			
RL	J. Biol. Chem. 263:14868-14877(1988).			
RN	[2]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=9213399; PubMed=3149637;			
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,			
RA	Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in bovine			
RT	blood coagulation factors VII and IX.";			
RL	J. Biochem. 104:867-868(1988).			
RN	[3]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=2129367;			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RL	Adv. Exp. Med. Biol. 281:121-131(1990).			
CC	-1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWMOGEN FORM. FACTOR VII IS			
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIA, FACTOR IXA, OR			
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR			
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA			
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO			
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR IX TO			
CC	-1- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to			
CC	form factor Xa.			
CC	-1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED			
CC	BY A DISULFIDE BOND.			
CC	-1- TISSUE SPECIFICITY: PLASMA.			
CC	-1- PM: THE VITAMIN K-DEPENDENT. ENZYMAIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.			
DR	PIR; A31979; A31979.			
DR	HSSP; P08709; 1BF9.			

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DR MEROPS; S01.215; -.
DR InterPro; IPR0000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0010; EGF_BLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Sec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KM Layer; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT DOMAIN 153 407 FACTOR VII HEAVY CHAIN.
FT ACT_SITE 193 193 GLA-RICH.
FT ACT_SITE 242 242 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).
FT BINDING 338 338 EGF-LIKE 2.
FT DISULFID 17 22 SUBSTRATE (BY SIMILARITY).
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

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OY 1 ANGFLLXLRNGSLKRXCRXXLCSFYXAFYIRNXXKRTQFWVS 44
DB 1 ANGFLEILLPSGLRECREDELCSFEAEHIFRNERTQFWVS 44

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg--Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; BAB37326.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR
DR

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Query March 77.0%; Score 147; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 1, 1e-16;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Query Match	Best Local Similarity	Score 127;	DB 1;	Length 444;
Matches 23;	Conservative 7;	Mismatches 14;	Indels 0;	Gaps 0;
Qy 1	ANGFLXKLRLNGSLXRXCRXXLCSFXKAFYIFRXIXXTRPOFWWSY 44			
Db 40	ANSFLEELRPGSLIRCKEELCSFEELAREVFGSTERTKQFWITY 83			
RESULT 3				
AC	FA7 HUMAN	STANDARD;	PRT;	466 AA.
DT	P08709; Q14339; 01-JAN-1988 (Rel. 06, Created)			

DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 conversion accelerator) (Eptacog alfa).
 GN F7.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86205965; PubMed=3486420;
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
 RA Davie E.W.;
 RT "Characterization of a cDNA coding for human factor VII.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260948; PubMed=3037537;
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
 RA Hagen F.S., Murray M.J.;
 RT "Nucleotide sequence of the gene coding for human factor VII, a
 RT vitamin K-dependent protein participating in blood coagulation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
 RA Rider M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=89088153; PubMed=3264725;
 RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
 RA Pedersen A.H., Hedner U.;
 RT "Amino acid sequence and posttranslational modifications of human
 RT factor VIIa from plasma and transfected baby hamster kidney cells.";
 RL Biochemistry 27:7785-7793(1988).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
 RX MEDLINE=91250411; PubMed=1904059;
 RA Bjoern S., Foster D.C., Thim L., Wberg F.C., Christensen M.,
 RA Komiyama Y., Pedersen A.H., Kistiel W.;
 RT "Human plasma and recombinant factor VII. Characterization of O-
 RT glycosylations at serine residues 52 and 60 and effects of site-
 RT directed mutagenesis of serine 52 to alanine.";
 RL J. Biol. Chem. 266:11051-11057(1991).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomura H., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT external growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
 RA "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 461
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 253 253
 FT ACT_SITE 299 299
 FT ACT_SITE 402 402
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 319
 FT DISULFID 238 254
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 214 214
 FT CARBOHYD 290 290
 FT CARBOHYD 355 355
 FT CONFLICT 328 328
 FT CONFLICT 393 393
 FT SEQUENCE 461 AA; 51945 MM; 53FAAD08B194D6E CRC64;
 Query March 53.9%; Score 103; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 9.1e-11;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

DT 01-NOV-1997 (Rel. 35, last sequence update)
 DE 15-NOV-2002 (Rel. 41, last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN F7 OR CF7.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 CX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene.";
 RL Thromb. Haemost. 76:957-964 (1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; U66079; AAC3396.1; -.
 DR HSSP; P08709; 1BP9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR000152; Asx hydroxy1.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; Trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM0069; GLA; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;


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FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 387 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 53.4%; Score 102; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.4e-10;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFIPNXXRTQFVWSY 44
DB 42 ANSFLEEVNAGSLERECEMEICDFEBOEIIFQVEDTLAFWKY 85

RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=21117044; PubMed=11719571;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF326350; AA00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLU_blood.
DR InterPro; IPR00294; VitK_dep_GLU.
DR Pfam; PF00594; Glu; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 231 PROTEIN 3
FT DOMAIN 79 101 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 102 231 POTENTIAL.
FT DOMAIN 23 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 60 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25648 MW; 8A373E4848490D81 CRC64;

Query Match 51.3%; Score 98; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.6e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFIPNXXRTQFVWSY 44
DB 20 ANSFLEEVNAGSLERECEMEICSYBEVKEVFNKRTMEFWKGY 63

RESULT 9
PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GUP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modelling of membrane binding sites and comparative anatomy of
RT domains.";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -----
```

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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 CC -----
 CC EMBL: AF191307; AAC28380.1; -.
 CC HSSP: P04070; 1PCT.
 CC MEROPS: S01.218; -.
 CC InterPro: IPR000152; Abx_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR001881; EGF Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC InterPro: IPR000294; Vitr_dep_GLA.
 CC Pfam: PF00008; EGF_2.
 CC Pfam: PF00089; trypsin_1.
 CC Pfam: PF00594; glaf_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00181; EGF_2.
 CC SMART: SM00001; EGF-like_2.
 CC SMART: SM00069; GLA_1.
 CC SMART: SM00020; Tryp_Spc_1.
 CC PROSITE: PS00010; ASX_HYDROXYL_1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF CA; 1.
 CC PROSITE: PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE: PS02040; TRYPSIN DOM; 1.
 CC PROSITE: PS00135; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Glycoprotein; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 CC SIGNAL: 1 18
 CC PROPEP 19 41
 CC CHAIN 42 459
 CC CHAIN 42 196
 CC CHAIN 199 459
 CC PEPTIDE. 199 213
 CC SITE 213 214
 CC DOMAIN 96 131
 CC DOMAIN 135 175
 CC DOMAIN 214 459
 CC MOD_RES 47 47
 CC MOD_RES 48 48
 CC MOD_RES 55 55
 CC MOD_RES 57 57
 CC MOD_RES 60 60
 CC MOD_RES 61 61
 CC MOD_RES 66 66
 CC MOD_RES 67 67
 CC MOD_RES 67 67

FT MOD_RES 70 70
 FT 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SO SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 51.3%; Score 98; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 7; 2e-10;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGFLXLRNGSLXKCRXKLCSPXAFIFRNXKTRQWVY 44
 DB 42 ANSFLERLRPSSLEBECKTCDFEARELFONTENTMAWSKY 85
 RESULT 10
 PA10_RABIT STANDARD; PRT; 490 AA.
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OK NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R.; Anderson K.D.; James H.L.;
 RL "Characterization of a full-length cDNA for rabbit factor X.",
 CC Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@ebi.ac.uk).

DR EMBL; AF003200; AAB62542.1; -
 DR HSP; P00742; IHG.
 DR MEROP; S01.216; -
 DR Interpro: IPR000152; Aax hydroxyl.
 DR Interpro: IPR001314; Chymotrypsin.
 DR Interpro: IPR000561; EGF-like.
 DR Interpro: IPR000742; EGF 2.
 DR Interpro: IPR01881; EGF-Ca.
 DR Interpro: IPR002383; GLA Blood.
 DR Interpro: IPR001254; Ser protease Try.
 DR Interpro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYATTN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Glycopolrotein. Hydrolyase: Serine protease; Plasma; Blood coagulation;
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat.
 FT PROPEP 1 20
 FT CHAIN 21 40
 FT CHAIN 41 180
 FT CHAIN 184 490
 FT PROPEP 184 232
 FT CHAIN 233 490
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 233 490
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66
 FT MOD_RES 69 69
 FT MOD_RES 72 72
 FT MOD_RES 75 75
 FT MOD_RES 79 79
 FT MOD_RES 103 103
 FT ACT_SITE 274 274

FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
 FT ACT_SITE 417 417 BY SIMILARITY.
 FT DISULFID 90 101 BY SIMILARITY.
 FT DISULFID 95 110 BY SIMILARITY.
 FT DISULFID 112 121 BY SIMILARITY.
 FT DISULFID 129 140 BY SIMILARITY.
 FT DISULFID 136 149 BY SIMILARITY.
 FT DISULFID 151 164 BY SIMILARITY.
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 239 244 BY SIMILARITY.
 FT DISULFID 259 275 BY SIMILARITY.
 FT DISULFID 388 402 BY SIMILARITY.
 FT DISULFID 413 441 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 50.3%; Score 96; DB 1; Length 490;
 Best Local Similarity 38.6%; Pred. No. 1.7e-09;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGLFLXLRNGSLKRCRXSLCSFXAFXIFRNXXRTROFVSVY 44
 Db 41 ANSLFELKKNLRECEMEENCSEALVEFDEKNEFNKKY 84

RESULT 11
 PRTC BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-JUN-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Antithrombin IIIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV) (Fragment).
 DE PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGallivray R.T.A.;
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RN [2]
 RP SEQUENCE OF 40-194.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RT "Amino acid sequence of the light chain of bovine protein C";
 RL J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RT "Amino acid sequence of the heavy chain of bovine protein C";
 RL J. Biol. Chem. 257:12180-12190(1982).
 RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.B., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 domainless protein C";

RL J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Esmon N.L., Lane T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 by Ca2+ binding to a high affinity site that does not contain gamma-
 carboxyglutamic acid."
 RL J. Biol. Chem. 258:5554-5560(1983).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 SITE IS NECESSARY FOR THE RECOGNITION OF THE
 THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: K02435; AAA30685.1; -.
 DR PIR: A00928; KXBO.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Aex_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; trypsin_1.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1_1.
 DR PROSITE: PS01186; EGF_2_2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS00240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00135; TRYPSIN_SER_1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT NON TER 1
 FT SIGNAL 1
 FT PROPEP 30
 FT CHAIN 40
 FT CHAIN 197
 FT PEPTIDE 197
 FT DOMAIN 94
 FT DOMAIN 133
 FT DOMAIN 211
 PROTEIN C LIGHT CHAIN.
 PROTEIN C HEAVY CHAIN.
 ACTIVATION PEPTIDE.
 EGF-LIKE 1.
 EGF-LIKE 2.
 SERINE PROTEASE.

FT MOD_RES 45
 FT MOD_RES 46
 FT MOD_RES 53
 FT MOD_RES 55
 FT MOD_RES 58
 FT MOD_RES 59
 FT MOD_RES 62
 FT MOD_RES 64
 FT MOD_RES 65
 FT MOD_RES 68
 FT MOD_RES 74
 FT MOD_RES 110
 FT ACT_SITE 252
 FT ACT_SITE 298
 FT ACT_SITE 397
 FT DISULFID 56
 FT DISULFID 89
 FT DISULFID 98
 FT DISULFID 102
 FT DISULFID 119
 FT DISULFID 137
 FT DISULFID 144
 FT DISULFID 159
 FT DISULFID 180
 FT DISULFID 237
 FT DISULFID 368
 FT DISULFID 393
 FT CARBOHYD 136
 FT CARBOHYD 289
 FT CARBOHYD 350
 FT CARBOHYD 366
 FT VARIANT 82
 FT CONFLICT 455
 SQ SEQUENCE 456 AA; 51407 MW; CAA6833F894C209 CRC64;
 Query Match 48.7%; Score 93; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 5,6e-09;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 1 ANGFLXLRNGSLKRYCRXKLCSEFYXAFIFRMXXRPFQWVSY 44
 40 ANSFLERLRGNVERECSEFEARELIFONTEDTMAWFSFY 83
 ID FA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 human coagulation factor X."
 RT Gene 99:291-294 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 organization is essentially identical with that of factor IX and
 protein C."
 RT Biochemistry 25:5098-5102(1986).
 RN [3]

RP SEQUENCE OF 13-488 FROM N.A.
 RP MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length CDNA coding for human
 RT blood coagulation factor X.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595 (1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildbrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RT Gene 41:311-314 (1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RP MEDLINE=83257207; PubMed=6871167;
 RA Mcullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884 (1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RP TISSUE=Liver;
 RC MEDLINE=8422026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702 (1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RA MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163 (1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RP MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameeshan K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519 (1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RP MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blenkenship D.T., Gardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966 (1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RP MEDLINE=98283982; PubMed=9618463;
 RA Kanata K., Kawamoto H., Horita T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635 (1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: K03194; AAA52490.1; -;
 CC EMBL: M57285; AAA52421.1; -;
 CC EMBL: L29433; AAA52764.1; -;
 CC EMBL: L00390; AAA52764.1; JOINED.
 CC EMBL: L00391; AAA52764.1; JOINED.
 CC EMBL: L00392; AAA52764.1; JOINED.
 CC EMBL: L00393; AAA52764.1; JOINED.
 CC EMBL: L00394; AAA52764.1; JOINED.
 CC EMBL: L00395; AAA52764.1; JOINED.
 CC EMBL: L00396; AAA52764.1; JOINED.
 CC EMBL: M22613; AAA51984.1; -;
 CC EMBL: K01886; AAA52486.1; -;
 CC EMBL: M33297; AAA52636.1; -;
 CC PIR: A00924; EXHU
 CC PIR: A25853; A25853.
 CC PIR: A24478; A24478.
 CC PDB: 1HCG; 08-MAY-95.
 CC PDB: 1FAX; 29-OCT-97.
 CC PDB: 1EXY; 17-JUN-98.
 CC PDB: 1XKA; 23-MAR-99.
 CC PDB: 1XKB; 23-MAR-99.
 CC MEROPS: S01.216; -;
 CC GlycoSiteDB: P00742; -;
 CC Genew: HGNC:3528; F10.
 CC MIM: 134530; -;
 CC MIM: 227600; -;
 CC InterPro: IPR000152; Nex_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF 2.
 CC InterPro: IPR001881; EGF Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR01254; Ser_protease_Try.
 CC InterPro: IPR00294; YltK_dep_GLA.
 CC Pfam: PF00008; EGF; 2.
 CC Pfam: PF00089; trypsin; 1.
 CC Pfam: PF00594; gla; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00179; EGF_CA; 1.
 CC SMART: SM00001; EGF_like; 1.
 CC SMART: SM00069; GLA; 1.
 CC SMART: PS00020; TRYD_SPC; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF_CA; 1.
 CC PROSITE: PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC GlycoSiteDB: Hydroxylase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; 3d-structure.
 CC SIGNAL: 1 31
 CC PROPEP: 32 40
 CC CHAIN: 41 179
 CC CHAIN: 183 488
 CC PROPEP: 183 234
 CC CHAIN: 235 488
 CC DOMAIN: 86 122
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).


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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT MOD_RES 103 103 O-LINKED (GLNAC. . .).
FT CARBOHYD 199 199 O-LINKED (GLNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 /FTID=CAR_000013.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 48.2%; Score 92; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 9e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

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QY 1 ANGLFLLRNGSLKRCXKXKSPXAFJFRNXXRTQFVSVY 44

Db 41 ANSFLPEMKKGLERECMETCTSYEARVEFDSKDTEFNWKKY 84

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RESULT 13
PRTC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (Ec 3.4.21.69)
DE (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=65270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN 2
RP SEQUENCE FROM N.A.
RX MEDLINE=65269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).
RN 3
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).

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RN 4
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN 5
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=64272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN 6
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J. Jr.;
RT "beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN 7
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN 8
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN 9
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganesyan V., Hof P., Huber R., Foundling S., Esmen C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN 10
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN 11
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staampfl S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN 12
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitlole A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN 13
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";

```

RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein C deficiency: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schliman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=92350852; PubMed=1301959;
 RA Gaudrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gaudrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsumita T., Sugita I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shitakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38, CYS-42, HIS-42, GLN-271 AND ASN-294.
 RX MEDLINE=9313192; PubMed=8324221;
 RA Gaudrille S., Alhenc-Gelas M., Gausem P., Allaud M.-F., Dupuy E.,
 RA Juhan-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poor S.R., Fabiner-Fasching I., Mannhalter C., Reitema P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous

RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koopman M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrachini P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 Query Match 47.1%; Score 90; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 1.9e-08;
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLKRXCRXXLCSPKXAFIRNXXRTQFW 41
 Db 43 ANSFLELRHSLRECEIEICDFEAKEIFQNVDDTLAFW 83
 RESULT 14
 FA10_BOVIN STANDARD; PRT; 492 AA.
 ID FA10_BOVIN
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor)."
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1993).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain."

Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 [5]
 RN SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=94062825; PubMed=8243461;
 RX Inoue K., Morita T.;
 RA "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson J.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:489-493(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCULUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxylglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the C2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96367194; PubMed=8794734;
 RA Sunnerhagen M., Olaf G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Tremella J.;
 RT "The relative orientation of Glu and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Thr and then
 CC Arg|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A00925; EXBO.
 CC PDB; IAPD; 31-JAN-94.
 CC PDB; ICCF; 31-MAY-94.
 CC PDB; IWHF; 15-MAY-97.
 CC PDB; IWHF; 15-MAY-97.
 CC MEROPS; S01.216; -.
 CC GlycoSuiteDB; P00743; -.
 CC InterPro; IPR000152; Asx_hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR007742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PR00008; EGF_2.
 CC Pfam; PR00089; trypsin; 1.
 CC Pfam; PR00594; gla; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxylglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3d-structure.
 CC SIGNAL 1 23
 CC PROPEP 24 40
 CC CHAIN 41 180
 CC CHAIN 183 492
 CC PROPEP 183 233
 CC CHAIN 234 492
 CC PROPEP 476 492
 CC DOMAIN 86 122
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR
 CC ACTIVATION.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

RL Biochemistry 27:9160-9165(1988).
 RN (17)
 RX VARIANT QUICK-2.
 MEDLINE=89247398; PubMed=2719946;
 RA Henrikson R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 thrombin Quick II alters primary substrate specificity.";
 RL Biochemistry 28:2078-2082(1989).
 RN (18)
 RP VARIANT SALAKTA.
 MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RX "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 reduces the fibrinogen clotting activity and the esterase activity.";
 RT Biochemistry 31:7457-7462(1992).
 RN (19)
 RP VARIANT TOKUSHIMA.
 MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawachi S., Shirakami A.,
 RX "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 that impairs the fibrinogen clotting activity of derived thrombin
 Tokushima.";
 RT Biochemistry 26:1117-1122(1987).
 RN (20)
 RP VARIANT TOKUSHIMA.
 MEDLINE=87101511; PubMed=3801671;
 RA Inomoto T., Shirakami A., Kawachi S., Shigekiyo T., Saito S.,
 RX Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 derived from a variant of human prothrombin.";
 RL Blood 69:565-569(1987).
 RN (21)
 RP VARIANT TOKUSHIMA.
 MEDLINE=92256895; PubMed=1349838;
 RA Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RX Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 Tokushima. The application of PCR-SSCP for the genetic and molecular
 analysis of dysprothrombinemia.";
 RL Int. J. Hematol. 55:93-100(1992).
 RN (22)
 RP VARIANT TYPE-3.
 MEDLINE=83204687; PubMed=6405779;
 RX Board P.G., Shaw D.C.;
 RA "Determination of the amino acid substitution in human prothrombin
 type 3 (157 Glu leads to Lys) and the localization of a third
 thrombin cleavage site.";
 RT Br. J. Haematol. 54:245-254(1983).
 RN (23)
 RP FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,
 AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,
 CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER. FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 OF PROTHROMBIN TO THROMBIN.
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 DYSPROTHROMBINEMIA.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
 THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 THROMBIN.
 CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION

CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 Query Match 45.0%; Score 86; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred.No. 1.4e-07;
 Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANGFLLXLRNGSLXRXCRXXLCSFXXAEXFFRXNXTTQPFWSY 44
 DB 44 ANTFLEVRKGNLRRCVETCTSYEAFFEALESSTATDVFWAKY 87

Search completed: March 19, 2003, 14:53:00
 Job time : 6.625 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLRNGLXRCRX.....XXAFYFRXXRTPFWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	62.3	701	4	Q96PQ8
2	103	53.9	460	11	Q91WN8
3	102	53.4	460	11	Q61109
4	97	50.8	460	11	Q99PC6
5	95	49.7	456	6	Q9TRK0
6	92	48.2	482	11	Q63207
7	89	46.6	481	11	Q54740
8	89	46.6	481	11	Q99132
9	89	46.6	481	11	Q88947
10	86	45.0	100	4	Q15253
11	86	45.0	608	13	Q9FTW7
12	85	44.5	49	6	Q95ME8
13	85	44.5	456	4	Q14316
14	85	44.5	461	6	Q95ND7
15	85	44.5	461	6	Q95ND6
16	85	44.5	469	6	Q9GMD9

17	78	40.8	138	6	Q28994	Q28994 sus scrofa
18	78	40.8	433	13	Q90YK1	Q90YK1 brachydanio
19	74	38.7	607	13	Q91001	Q91001 gallus gall
20	72	37.7	648	6	Q29094	Q29094 sus scrofa
21	71	37.2	399	11	Q9COW3	Q9COW3 mus musculus
22	68.5	35.9	542	5	Q8TEI3	Q8TEI3 halocynthia
23	67	35.1	179	4	Q8TAS3	Q8TAS3 homo sapien
24	67	35.1	198	11	Q8TAS3	Q8TAS3 homo sapien
25	67	35.1	650	4	Q9NSD0	Q9NSD0 homo sapien
26	67	35.1	650	4	Q16519	Q16519 homo sapien
27	57	29.8	25	11	Q9QVH6	Q9QVH6 rattus sp.
28	56	29.3	678	11	Q14393	Q14393 homo sapien
29	55	28.8	673	11	Q61592	Q61592 mus musculus
30	55	28.8	674	11	Q99K57	Q99K57 mus musculus
31	53	27.7	98	13	P82807	P82807 notechis sc
32	53	27.7	674	11	Q63772	Q63772 rattus sp.
33	52	27.2	249	5	Q9VYS0	Q9VYS0 drosophila
34	51	26.7	130	12	Q9DUB8	Q9DUB8 tt virus
35	50	26.2	184	10	Q9LVF1	Q9LVF1 arabidopsis
36	49	25.7	1217	5	Q9XV62	Q9XV62 caenorhabdi
37	48	25.1	472	13	Q98SU5	Q98SU5 gaetereosteu
38	48	25.1	613	13	Q98SU5	Q98SU5 gaetereosteu
39	48	25.1	910	13	Q98SU7	Q98SU7 gaetereosteu
40	47.5	24.9	575	10	Q94E17	Q94E17 oryza sativ
41	47.5	24.9	608	10	Q9XF36	Q9XF36 medicago sa
42	46.5	24.3	196	10	Q04284	Q04284 seleginella
43	46.5	24.3	567	10	Q8W4J2	Q8W4J2 arabidopsis
44	46.5	24.3	603	10	Q9LPG7	Q9LPG7 arabidopsis
45	46.5	24.3	606	10	Q95UG9	Q95UG9 arabidopsis

ALIGNMENTS

RESULT 1

Q96PQ8 PRELIMINARY; PRT; 701 AA.

ID Q96PQ8

AC Q96PQ8; 01-DRC-2001 (T-REMBLrel. 19, Created)

DT 01-DRC-2001 (T-REMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (T-REMBLrel. 20, Last annotation update)

DE Factor VII active site mutant immunocoujugate.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

ON NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.; PubMed=11593034;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

DR EMBL; AF272774; AAKS686.1; -

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VltK_dep_GLA.

DR Pfam; PRF00008; EGF; 2.

DR Pfam; PRF00594; G1a; 1.

DR Pfam; PRF0047; IG; 2.

DR Pfam; PRF0089; trypsin; 1.

DR SMART; SMO0181; EGF; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; UNKNOWN_1.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94ACCEB42CC992F CRC64;

Query Match 62.3%; Score 119; DB 4; Length 701;
 Best Local Similarity 52.3%; Pred. No. 4.4e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIFRNXXRTROFWVS 44
 Db 61 ANAFLEELRPGSLERECKEBOCSFEAREIFDARITKLFWISY 104

RESULT 2

ID 091NM8 PRELIMINARY; PRT; 460 AA.
 AC 091NM8;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RL Strauberg R.;
 RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013896; AAH13896.1; -.
 DR MGD; MGI:97771; Proc.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS02440; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydrolyase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E6FCC274 CRC64;

Query Match 53.9%; Score 103; DB 11; Length 460;
 Best Local Similarity 45.5%; Pred. No. 2.5e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIFRNXXRTROFWVS 44
 Db 42 ANSLLEEMRPGSLERECKEBOCSFEAREIFDARITKLFWISY 85

RESULT 3

ID 061109 PRELIMINARY; PRT; 446 AA.
 AC 061109;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Coagulation factor VII.
 GN F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idsogile E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castelli F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII,"
 CC Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY

CC EMBL; U44795; AAC52570.1; -.
 DR HSSP; P08709; 1FAK.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR01314; Chymotrypsin.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR00294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS00022; CRYSTALLIN_BETGAMMA; UNKNOWN_1.
 DR PROSITE; PS00025; CRYSTALLIN_BETGAMMA; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS02440; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 53.4%; Score 102; DB 11; Length 446;
 Best Local Similarity 47.7%; Pred. No. 3.6e-10;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIFRNXXRTROFWVS 44
 Db 42 ANSLLEELRPGSLERECKEBOCSFEAREIFKSPRTIKFWIV 85

RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.
 AC 099PC6;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;


```
RT "Complete sequence of UC72A01."
RU Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MG1:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; GLA; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_1like; 2.
DR SMART; SM00069; EGF_1like; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 3.1e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLKRCRXKLCSPFXAFXIFRNXXRTQRFVSY 44
DB 42 ANSLFLEMRPSLRECEMEICDLEAQEIFQVNDTLAYWSKY 85

RESULT 5
Q9TRR0 PRELIMINARY; PRT; 456 AA.
AC Q9TRR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein C precursor.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunnberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9371952; Pubmed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238 (1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
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DR EMBL; AJ001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; GLA; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192
FT CHAIN 193 194
FT CHAIN 195 456
FT CHAIN 195 456
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E55FF CRC64;

Query Match 49.7%; Score 95; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 7e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLKRCRXKLCSPFXAFXIFRNXXRTQRFVSY 44
DB 43 ANSLFLEMRPSLRECEMEICDLEAQEIFQVNDTLAYWSKY 86

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY;
RC MEDLINE=96093366; Pubmed=8578539;
RA Stanton C., Rose R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73 (1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1YXA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000294; VitK_dep_GLA.
DR InterPro; IPR000294; VitK_dep_GLA.
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DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF000069; GLA; 1.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase;
DR Hydroxylation; Repeat; Serine protease
KW SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.2%; Score 92; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 2.6e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLKRCXKXLCSEFXKXAFIRNXXRTQFWVSY 44

Db 41 ANSFEEFKGNLERECVEICSEFEAREVEFEDNEKTTEFWNKY 84

RESULT 7

OS4740 PRELIMINARY; PRT; 481 AA.

ID OS4740
AC OS4740; PRELIMINARY; PRT; 481 AA.
DT 01-JUN-1998 (TREMBlrel. 06; Created)
DT 01-JUN-1998 (TREMBlrel. 06; Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21; Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F410.
OS Mus musculus (Mouse).
OC Plasmid DBLuscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 41
FT SEQUENCE 481 AA; 53986 MW; CF702DBE5EF9D97AE CRC64;

Query Match 46.6%; Score 89; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 9.2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLKRCXKXLCSEFXKXAFIRNXXRTQFWVSY 44

Db 41 ANSFEEFKGNLERECVEICSEFEAREVEFEDNEKTTEFWNKY 84

RESULT 8

Q99L32 PRELIMINARY; PRT; 481 AA.

ID Q99L32
AC Q99L32;
DT 01-JUN-2001 (TREMBlrel. 17; Created)
DT 01-JUN-2001 (TREMBlrel. 17; Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21; Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

[illegible]

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OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio
OX NCBI_Taxid=8801;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20579470; PubMed=1137455;
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
RT "Participation and characterization of ostrich prochrombin.";
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB028871; BAA89046.1; -.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Ser. protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00051; Kringle_2.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRODOM: PD000395; Kringle_2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR HydroLase: Serine protease.
SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;

Query Match 45.0%; Score 86; DB 13; Length 608;
Best Local Similarity 35.7%; Pred. No. 4.1e-07;
Matches 15; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 3 GFLXXLRNGSLXRCRXLYLCSFXAXFIFFNNXXRTROPFWVS 44
Db 47 GFLLEMLKGNLERECLEICIEEFALESTARTEEFWSKY 88

RESULT 12
Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF394598; AAK7556.1; -.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 49 AA; 6023 MW; DISC6DB9CBA4A14 CRC64;
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Query Match 44.5%; Score 85; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 5.2e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRNGSLXRCRXLYLCSFXAXFIFFNNXXRTROPFWVS 44
Db 6 SGKLEEFVRGNLERECKSEKSFEEARREVFENTKTETFWQY 48

RESULT 13
Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1999 (TREMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas
DE disease HAEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AL033403; CAA21954.1; -.
DR EMBL: X55008; CAB38245.2; -.
DR HSSP: P00740; ICEH.
DR MEROPS: S01.214; -.
DR InterPro: IPR000152; Aex hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR00742; EGF_2.
DR InterPro: IPR00742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Ser. protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBLD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 44.5%; Score 85; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 4.7e-07;
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Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
QY 2 NGFLXLRNGSLKRXCRXXLCSFXXAFXIFRNXXRTROFWVSY 44
DB 44 SGKLEEFVQGNLERECMEKCSFEAREVFEINTERTEFWKQY 86

RESULT 14

Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7, 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor XI.
GN Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
chimpanzees.";
RL Genes Genet. Syst. 0.0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_Protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2P857C0P77F45 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 4.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXLRNGSLKRXCRXXLCSFXXAFXIFRNXXRTROFWVSY 44
DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFEINTERTEFWKQY 91

RESULT 15
Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6, 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor XI.
GN Pan troglodytes (Chimpanzee).
OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
chimpanzees.";
RL Genes Genet. Syst. 0.0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_Protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 4.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
QY 2 NGFLXLRNGSLKRXCRXXLCSFXXAFXIFRNXXRTROFWVSY 44
DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFEINTERTEFWKQY 91

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OM protein - protein search, using sw model

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	80.6	44	3	US-08-955-636-4
2	128	67.0	44	3	US-08-955-636-28
3	122	63.9	44	3	US-08-955-636-27
4	121	63.4	44	3	US-08-955-636-26
5	119	62.3	44	3	US-08-955-636-3
6	119	62.3	44	3	US-08-955-636-30
7	119	62.3	406	1	US-08-293-778-24
8	119	62.3	406	1	US-08-295-411-5
9	119	62.3	406	2	US-08-955-471-5
10	119	62.3	406	5	PCT-US92-10242-5
11	119	62.3	444	1	US-08-475-945-2
12	119	62.3	444	2	US-08-327-590-2
13	119	62.3	444	2	US-08-660-289-2
14	119	62.3	444	2	US-08-537-807-2
15	119	62.3	444	2	US-08-871-003-2
16	119	62.3	444	3	US-08-464-233-2
17	119	62.3	444	4	US-08-189-607-2
18	119	62.3	444	4	US-09-378-907-2
19	119	62.3	444	5	PCT-US94-05779-2
20	119	62.3	466	1	US-07-882-202A-4
21	119	62.3	466	1	US-08-021-615A-4
22	119	62.3	466	1	US-08-321-777-4
23	119	62.3	466	4	US-09-009-217-14
24	119	62.3	466	4	US-09-009-556-14
25	119	62.3	466	5	PCT-US93-04493-4
26	115	60.2	44	3	US-08-955-636-29
27	105	55.0	41	1	US-08-229-280-4

28	97	50.8	139	1	US-08-330-978-2	Sequence 2, Appl
29	97	50.8	139	1	US-08-474-042-2	Sequence 2, Appl
30	97	50.8	139	1	US-08-484-558-2	Sequence 2, Appl
31	97	50.8	139	1	US-08-774-592-2	Sequence 2, Appl
32	97	50.8	437	1	US-08-487-037-2	Sequence 2, Appl
33	97	50.8	437	1	US-08-487-037-3	Sequence 3, Appl
34	97	50.8	488	1	US-08-487-037-1	Sequence 1, Appl
35	96	50.3	44	3	US-08-955-636-23	Sequence 23, Appl
36	93	48.7	44	3	US-08-955-636-25	Sequence 25, Appl
37	93	48.7	44	3	US-08-295-411-3	Sequence 3, Appl
38	92	48.2	448	1	US-08-955-471-3	Sequence 3, Appl
39	92	48.2	448	5	PCT-US92-10068-1	Sequence 1, Appl
40	92	48.2	448	5	PCT-US92-10242-3	Sequence 3, Appl
41	92	48.2	448	5	PCT-US92-10242-5	Sequence 5, Appl
42	90	47.1	41	1	US-08-229-280-5	Sequence 2, Appl
43	90	47.1	42	2	US-08-745-254A-2	Sequence 2, Appl
44	90	47.1	44	3	US-08-955-636-1	Sequence 1, Appl
45	90	47.1	45	2	US-08-965-832-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; CURRENT APPLICATION NUMBER: US/08/955,636A
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      80.6%; Score 154; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 6.6e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCFXAXAFXIFRNXXRTQFWVSY 44
Db 1 ANGFLXXLRNGSLRXCRXXLCFXAXAFXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; CURRENT APPLICATION NUMBER: US/08/955,636A
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match 67.0%; Score 128; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 2,1e-15;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Db 1 ANAFLXLRPGSLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 3

US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match 63.9%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2,4e-14;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLXLRDGSRLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 4

US-08-955-636-26
Sequence 26, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 63.4%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3,5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLXLRREGSLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 5

US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match 62.3%; Score 119; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,8e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLXLRPSGLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 6

US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 62.3%; Score 119; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,8e-14;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLXLRQGSRLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 7

US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560

GENERAL INFORMATION:
APPLICANT: Nicolaissen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Rinn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 55805600disk of No. 55805600th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match 62.3%; Score 119; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCRXKXFXIFRNXXRTROFVSY 44
DB 1 ANAFLYLRPGSLYRCYKVCSPFYARFYKDAVRTLFWISY 44

RESULT 8
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 62.3%; Score 119; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCRXKXFXIFRNXXRTROFVSY 44
DB 1 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTLFWISY 44

RESULT 9
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA

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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: T5R1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 62.3%; Score 119; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRLNGSLKRXCRXLCSPFXAXIFRNXXRTQFWVSY 44
DB 1 ANAFLELRPGSLRECKEBCQSFPEARIRFDARTKLFWISY 44

RESULT 10
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Messers, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
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FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 62.3%; Score 119; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRLNGSLKRXCRXLCSPFXAXIFRNXXRTQFWVSY 44
DB 1 ANAFLELRPGSLRECKEBCQSFPEARIRFDARTKLFWISY 44

RESULT 11
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
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;; FILING DATE: 21-MAY-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/662,920
;; FILING DATE: 28-FEB-1991
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-475-845-2

Query Match 62.3%; Score 119; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 8,8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12

;; Sequence 2, Application US/08327690
;; Patent No. 5817788

;; GENERAL INFORMATION:
;; APPLICANT: Berkner, Kathleen L.
;; APPLICANT: Petersen, Lars C.
;; APPLICANT: Hart, Charles E.
;; APPLICANT: Hedner, Ulla
;; APPLICANT: Bregengaard, Claus
;; TITLE OF INVENTION: Modified Factor VII
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: One Market Plaza, Stewart Street Tower
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 94105-1492

COMPUTER READABLE FORM:

;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/327,690
;; FILING DATE: 24-OCT-1994

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/065,725
;; FILING DATE: 21-MAY-1993

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/662,920
;; FILING DATE: 28-FEB-1991

;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 13952-8-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-327-690-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8,8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13

;; Sequence 2, Application US/08660289
;; Patent No. 5833982

;; GENERAL INFORMATION:
;; APPLICANT: Berkner, Kathleen L.
;; APPLICANT: Petersen, Lars C.
;; APPLICANT: Hart, Charles E.
;; APPLICANT: Hedner, Ulla
;; APPLICANT: Bregengaard, Claus
;; TITLE OF INVENTION: Modified Factor VII
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: One Market Plaza, Stewart Street Tower
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 94105-1492

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/660,289
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/475,845
;; FILING DATE: 07-JUN-1995

;; APPLICATION NUMBER: 08/327,690
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/065,725
;; FILING DATE: 21-MAY-1993

;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/662,920
;; FILING DATE: 28-FEB-1991

;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 13952-8-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-660-289-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLKRXCRXXLCSFXAXFIFRNXXRTROFWVSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYLFWISY 82

RESULT 14
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLKRXCRXXLCSFXAXFIFRNXXRTROFWVSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYLFWISY 82

RESULT 15
; Sequence 2, Application US/08671003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-003-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLKRXCRXXLCSFXAXFIFRNXXRTROFWVSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYLFWISY 82

Search completed: March 19, 2003, 15:16:21
Job time : 9.75 secs

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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLLXRLRGLRXXCRXX.....XXAFXIFRXXRTQFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/prodata/2/pubppa/PC7_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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- 5: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
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- 9: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	62.3	406	9	US-10-109-498-1
2	90	47.1	419	9	US-10-182-263-1
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4	90	47.1	419	9	US-10-182-263-4
5	90	47.1	419	9	US-10-182-263-5
6	90	47.1	419	9	US-09-978-917A-4
7	90	47.1	461	9	US-10-182-263-2
8	90	47.1	461	9	US-09-978-917A-2
9	89	46.6	419	9	US-10-182-263-6
10	85	44.5	415	10	US-09-118-748-2
11	85	44.5	461	9	US-09-132-829-5
12	85	44.5	461	9	US-09-884-901-3
13	67	35.1	96	9	US-09-759-1308-313
14	67	35.1	209	9	US-09-759-1308-312
15	67	35.1	226	9	US-09-759-1308-310
16	50	26.2	95	9	US-09-759-1308-356
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18	50	26.2	225	9	US-09-759-1308-353
19	40	20.9	197	9	US-10-076-622-516

20	40	20.9	197	12	US-10-007-805-516	Sequence 516, App
21	40	20.9	232	9	US-10-076-622-517	Sequence 517, App
22	40	20.9	232	12	US-10-007-805-517	Sequence 517, App
23	40	20.9	243	9	US-09-938-418-7	Sequence 7, Appl
24	40	20.9	243	9	US-10-045-992-4	Sequence 4, Appl
25	40	20.9	243	9	US-10-063-547-122	Sequence 122, App
26	40	20.9	243	9	US-10-174-590-366	Sequence 366, App
27	40	20.9	243	9	US-10-176-758-366	Sequence 366, App
28	40	20.9	243	9	US-10-063-616-122	Sequence 122, App
29	40	20.9	243	9	US-10-176-737-366	Sequence 366, App
30	40	20.9	243	9	US-10-063-502-122	Sequence 122, App
31	40	20.9	243	9	US-10-076-622-514	Sequence 514, App
32	40	20.9	243	9	US-10-173-706-366	Sequence 366, App
33	40	20.9	243	9	US-10-175-738-366	Sequence 366, App
34	40	20.9	243	9	US-10-175-752-366	Sequence 366, App
35	40	20.9	243	9	US-10-176-482-366	Sequence 366, App
36	40	20.9	243	9	US-10-176-757-366	Sequence 366, App
37	40	20.9	243	9	US-10-176-913-366	Sequence 366, App
38	40	20.9	243	9	US-10-180-552-366	Sequence 366, App
39	40	20.9	243	9	US-10-180-557-366	Sequence 366, App
40	40	20.9	243	9	US-10-173-700-366	Sequence 366, App
41	40	20.9	243	9	US-10-174-572-366	Sequence 366, App
42	40	20.9	243	9	US-10-174-579-366	Sequence 366, App
43	40	20.9	243	9	US-10-174-582-366	Sequence 366, App
44	40	20.9	243	9	US-10-174-588-366	Sequence 366, App
45	40	20.9	243	9	US-10-175-739-366	Sequence 366, App

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286-200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      62.3%; Score 119; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 1.1e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Cy 1 ANGFLLXRLRGLRXXCRXXLCFFXAFXIFRXXRTQFWISY 44
Db 1 ANGFLLXRLRGLRXXCRXXQCSFFXAFXIFKDXAKRTKFWISY 44

RESULT 2
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bryce E
; APPLICANT: Jones, Bryan E
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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXFIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFDVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXFIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFDVDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXFIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFDVDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXFIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFDVDDTLAFW 41

RESULT 6
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219a8310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
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GenCore version 5.1.4 p5 4578
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3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds

(without alignments)
328.082 Million cell updates/sec

Title: 10GLN28GLU

Perfect score: 190
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	466	1	FA7_HUMAN
2	125	65.8	444	1	FA7_RABIT
3	115	60.5	407	1	FA7_BOVIN
4	114	60.0	446	1	FA7_MOUSE
5	102	53.7	461	1	PRTG_MOUSE
6	102	53.7	492	1	FA10_BOVIN
7	101	53.2	459	1	PRTG_PIG
8	101	53.2	461	1	PRTG_RAT
9	100	52.6	218	1	TMG1_HUMAN
10	99	52.1	488	1	FA10_HUMAN
11	93	48.9	231	1	TMG3_HUMAN
12	93	48.9	231	1	FA9_HUMAN
13	92	48.4	475	1	PRTG_BOVIN
14	91	47.9	456	1	PRTG_BOVIN
15	85	44.7	458	1	PRTG_RABIT
16	85	44.7	461	1	PRTG_HUMAN
17	85	44.7	622	1	THRB_HUMAN
18	83	43.7	461	1	FA9_HUMAN
19	82	43.2	416	1	FA9_BOVIN
20	81	42.6	618	1	THRB_MOUSE
21	81	42.6	618	1	THRB_MOUSE
22	79	41.6	376	1	FA10_HUMAN
23	76	40.0	202	1	TMG2_HUMAN
24	74	38.9	452	1	FA9_HUMAN
25	74	38.9	452	1	FA9_HUMAN
26	69.5	36.6	226	1	TMG4_HUMAN
27	65	34.2	625	1	THRB_BOVIN
28	65	34.2	649	1	PRTS_HUMAN
29	65	34.2	676	1	PRTS_HUMAN
30	63	33.2	675	1	PRTS_BOVIN
31	61	32.1	646	1	PRTS_BOVIN
32	61	32.1	646	1	PRTS_BOVIN
33	60	31.6	675	1	PRTS_RABIT

34	56	29.5	400	1	PRT2_HUMAN
35	53	27.9	675	1	PRTS_MOUSE
36	45	23.7	879	1	YN65_YEAST
37	44	23.2	413	1	NCAP_IHNV
38	43.5	22.9	322	1	YOL3_CARBL
39	42	22.1	263	1	PFLA_STRMU
40	41.5	21.8	271	1	MD12_YEAST
41	41.5	21.8	1290	1	BXB_CLOBO
42	40	21.1	341	1	MURB_PASMU
43	40	21.1	343	1	HMD_METYO
44	40	21.1	353	1	HMD_METTU
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ALIGNMENTS

RESULT 1	FA7_HUMAN	STANDARD;	PRT;	466 AA.
AC	P08709; 014339;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).			
DN	F7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=86205965; PubMed=3486420;			
RA	Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,			
RA	Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,			
RA	Davie B.W.;			
RT	"Characterization of a cDNA coding for human factor VII."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=87260948; PubMed=3037537;			
RX	O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,			
RA	Hagen F.S., Murray M.J.;			
RT	"Nucleotide sequence of the gene coding for human factor VII, a			
RT	vitamin K-dependent protein participating in blood coagulation."			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.			
RA	Rieder M.U., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Poel C.L., Toch E.J., Yi Q., Nickerson D.A.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.			
RX	MEDLINE=89088153; PubMed=3264725;			
RA	Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T.,			
RA	Pedersen A.H., Hedner U.;			
RT	"Amino acid sequence and posttranslational modifications of human			
RT	factor VIIa from plasma and transfected baby hamster kidney cells."			
RL	Biochemistry 27:7785-7793(1988).			
RN	[5]			
RP	CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.			
RX	MEDLINE=91250411; PubMed=1904059;			
RA	Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,			
RA	Komiyama Y., Pedersen A.H., Kistiel W.;			
RT	"Human plasma and recombinant factor VII. Characterization of O-			
RT	glycosylations at serine residues 52 and 60 and effects of site-			
RT	directed mutagenesis of serine 52 to alanine."			
RL	J. Biol. Chem. 266:11051-11057(1991).			
RN	[6]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-112.			
RX	MEDLINE=90062160; PubMed=2511201;			

RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN (17)
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN (18)
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903; Winkler F.K., Guha A.,
 RA Banner D.W., D'Arcy A., Chene C., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN (19)
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN (10)
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Murenki A., Finn B.E., Gispert G.P., Forssen S., Stenflo J.,
 RT Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN (11)
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RT Weade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN (12)
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccchini P., Derosa V., Pinotti M.,
 RT Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN (13)
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN (14)
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N.,
 RA von Felten A., Mellis E., Hahn I., Prangnell D.R., Lumley H.,
 RT Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN (15)
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chahng S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blatchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN (16)
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN (17)
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN (18)
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN (19)
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN (20)
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN (21)
 RP VARIANTS MULTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN (22)
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
 CC produced by alternative splicing.
 CC TISSUE SPECIFICITY: PLASMA.
 CC PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1.4e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 44
Db 61 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 104

RESULT 2
ID_FAT_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."
RL Thromb. Res. Suppl. 69:231-236(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U77477; AAB37326.1; -.
CC HSSP; P08709; IFAK.
DR INTERPRO; IPR000152; ASX_hydroxyl.
DR INTERPRO; IPR001314; Chymotrypsin.
DR INTERPRO; IPR000561; EGF-like.
DR INTERPRO; IPR000742; EGF_2.
DR INTERPRO; IPR001881; EGF_Ca.
DR INTERPRO; IPR002383; GLA_blood.
DR INTERPRO; IPR001254; Ser_protease_Try.

DR INTERPRO; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; signal; Hydroxylation.
KW EGF-like domain; Repeat; signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 65.8%; Score 125; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 1.6e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 44
Db 40 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 83

RESULT 3

RA7_BOVIN
 ID FA7_BOVIN STANDARD; PRT; 407 AA.
 AC P22457;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 GN F7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX [1]
 RX MEDLINE=89008362; PubMed=3049594;
 RA Takaya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.,
 "Bovine factor VII. Its purification and complete amino acid sequence."
 RT J. Biol. Chem. 263:14868-14877(1988).
 RL [2]
 RN STRUCTURE OF CARBOHYDRATE ON SER-52.
 RP MEDLINE=89213599; PubMed=3149637;
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.,
 "A new triasaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
 RT J. Biochem. 104:867-868(1988).
 RN [3]
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.
 RA MEDLINE=9144709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
 "A new triasaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
 RT Adv. Exp. Med. Biol. 281:121-131(1990).
 RL
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC PIR: A31979; A31979.
 DR HSPF; P08709; I18F9.
 DR MEROPS; S01.215; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF-2.
 DR InterPro; IPR001861; EGF-Ga.
 DR InterPro; IPR001438; EGF-11.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFbLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.

DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYPSIN; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_SER; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.
 KM EGF-like domain; Repeat.
 FT CHAIN 1 152
 FT CHAIN 153 407
 FT DOMAIN 6 35
 FT DOMAIN 46 82
 FT DOMAIN 87 128
 FT DOMAIN 153 407
 FT SITE 152 153
 FT ACT_SITE 193 193
 FT ACT_SITE 242 242
 FT ACT_SITE 344 344
 FT BINDING 338 338
 FT DISULFID 17 22
 FT DISULFID 50 61
 FT DISULFID 55 70
 FT DISULFID 72 81
 FT DISULFID 91 102
 FT DISULFID 98 112
 FT DISULFID 114 127
 FT DISULFID 135 262
 FT DISULFID 159 164
 FT DISULFID 178 194
 FT DISULFID 310 329
 FT DISULFID 340 368
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 14 14
 FT MOD_RES 16 16
 FT MOD_RES 19 19
 FT MOD_RES 20 20
 FT MOD_RES 25 25
 FT MOD_RES 26 26
 FT MOD_RES 29 29
 FT MOD_RES 35 35
 FT MOD_RES 52 52
 FT CARBOHYD 145 145
 FT CARBOHYD 203 203
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
 Query Match 60.5%; Score 115; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 8,6e-13;
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFPDAXRTKLFWSY 44
 DB 1 ANGFLEELPGLSLERECRELCSFEAEHIFRNEERTQRFWSY 44
 RESULT 4
 FA7_MOUSE STANDARD; PRT; 446 AA.
 ID FA7_MOUSE
 AC P70375;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 GN F7 OR CF7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RT Idusogie E., Rosen E.D., Carmeliet P., Collen D., Caetellino F.J.;
 "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWMOGEN FORM. FACTOR VII IS
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 SIMILARITY)
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT. ENZYMAIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@ebi.ac.uk).

CC -----
 DR EMBL; U66079; AAC33796.1; -.
 DR HSBP; P08709; 1BF9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI.109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Glai; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL; 1 24 POTENTIAL.
 FT PROPEP; 25 41 POTENTIAL.
 FT CHAIN; 42 193 FACTOR VII LIGHT CHAIN.
 FT DOMAIN; 194 446 FACTOR VII HEAVY CHAIN.
 FT DOMAIN; 47 76 GLA-RICH.
 FT DOMAIN; 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN; 128 169 EGF-LIKE 2.
 FT DOMAIN; 194 446 SERINE PROTEASE.
 FT SITE; 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,
 FT ACT_SITE; 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE; 283 283 BY SIMILARITY.
 FT ACT_SITE; 385 385 BY SIMILARITY.
 FT BINDING; 379 379 SUBSTRATE (BY SIMILARITY).
 FT DISULFID; 58 63 BY SIMILARITY.
 FT DISULFID; 91 102 BY SIMILARITY.
 FT DISULFID; 96 111 BY SIMILARITY.
 FT DISULFID; 113 122 BY SIMILARITY.
 FT DISULFID; 132 143 BY SIMILARITY.
 FT DISULFID; 139 153 BY SIMILARITY.
 FT DISULFID; 155 168 BY SIMILARITY.
 FT DISULFID; 176 303 BY SIMILARITY.
 FT DISULFID; 200 303 BY SIMILARITY.
 FT DISULFID; 219 235 BY SIMILARITY.
 FT DISULFID; 351 370 BY SIMILARITY.
 FT DISULFID; 381 409 BY SIMILARITY.
 FT MOD_RES; 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES; 104 104 GAMMA-CARBOXYGLUTAMIC ACID.
 FT CARBOHYD; 186 186 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD; 244 244 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 446 AA; 50276 MW; 251254445C9C95E CRC64;

Query Match 60.0%; Score 114; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 1,4e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFPLXIRGSGSLKRXCKXGCSFKXAEIRFKDAXRTLPFIISY 44
 Db 42 ANSLLEELMPGSLRECEECSEFEAREIFKSPERTKQFIWIV 85

RESULT 5
 ID PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
 factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 "Isolation and characterization of a mouse protein C cDNA."
 RT J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 Caetellino F.J.;
 "Nucleotide structure and characterization of the murine gene encoding

FT	SIGNAL	1	33	BY SIMILARITY.
FT	PROPEP	34	41	BY SIMILARITY.
FT	CHAIN	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199	461	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199	212	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	212	213	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	213	461	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48	48	(BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	57	57	(BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	60	60	(BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	61	61	(BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	66	66	(BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	67	67	(BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70	70	(BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253	253	CHARGE RELAY SYSTEM.
FT	ACT_SITE	299	299	CHARGE RELAY SYSTEM.
FT	ACT_SITE	402	402	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	319	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	238	254	BY SIMILARITY.
FT	DISULFID	373	387	BY SIMILARITY.
FT	DISULFID	398	426	BY SIMILARITY.
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328	328	MISSING (IN REF. 2).
FT	CONFLICT	393	393	N -> D (IN REF. 2).
SO	SEQUENCE	461 AA;	51945 MW;	53FMA0D85B194D6E CXC64;
Query Match 53.7%; Score 102; DB 1; Length 461;				
Best Local Similarity 45.5%; Pred. No. 2e-10;				
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;				
QY	1 ANAFXLARQGLRXCKXKXGCSFFXKXERIFPDARTKLFWSY 44			
DB	42 ANSFLEMRPGSLERECWEIICDFEEAOEIFQNVEDTLAFWIKY 85			
RESULT 6				
FA10_BOVIN	STANDARD;	PRT;	492 AA.	
AC	P00743;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cosguination factor X precursor (EC 3.4.21.6) (Stuart factor).			
GN	F10.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxId=9913;			

[1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN (2)
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Entfeld D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Tlani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";
 RL Biochemistry 19:659-667(1980).
 RN (3)
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN (4)
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Tlani K., Fujikawa K., Entfeld D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN (5)
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (6)
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Tlani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN (7)
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Tlani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN (8)
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Björk I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN (9)
 RP SUPPATION
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN (10)
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of

RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN (11)
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Telemann O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN (12)
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN (13)
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olaf G.A., Stenflo J., Foren S., Drakenberg T.,
 RA Trehwella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -I- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- PM: N- AND O-GLYCOSYLATED.
 CC -I- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC DR EMBL; X00673; CA25286.1; -.
 CC DR PIR; A00925; EXBO.
 CC DR PDB; IAPC; 31-JAN-94.
 CC DR PDB; IJCF; 31-JAN-94.
 CC DR PDB; IMHE; 15-MAY-97.
 CC DR PDB; IMHF; 15-MAY-97.
 CC DR MEROPS; S01.216; -.
 CC DR GlycosSiteDB; P00743; -.
 CC DR InterPro; IPR000152; Aex hydroxyl-
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR00742; EGF_2.
 CC DR InterPro; IPR001881; EGF_Ca.
 CC DR InterPro; IPR002383; Gla_Blood.
 CC DR InterPro; IPR001254; Ser protease_Try.
 CC DR InterPro; IPR000294; VitK_dep_GLA_

FT		96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	SERINE PROTEASE.
FT	DOMAIN	214	459	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	255	255	CHARGE RELAY SYSTEM.
FT	ACT_SITE	301	301	CHARGE RELAY SYSTEM.
FT	ACT_SITE	400	400	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	182	321	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	240	256	BY SIMILARITY.
FT	DISULFID	371	385	BY SIMILARITY.
FT	DISULFID	396	424	BY SIMILARITY.
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	459 AA;	8541AAC14CC16D09 CRC64;	
<hr/>				
Query Match				
Best Local Similarity		53.2%;	Score 101; DB 1; Length 459;	
Matches 20; Conservative		45.5%;	Pred. No. 3e-10; Indels 0; Gaps 0;	
		3; Mismatches 21;		
Oy	1 ANAFIXLRQGSILRXCKXXCSPFXAXEYIFDARKTKLFWSY 44			
Db	42 ANSFLEELRPSLSRECKEETCDPEBARITFOENTMFMFSKY 85			
<hr/>				
RESULT 8				
PRTC_RAT	ID_PRTC_RAT	STANDARD;	PRT;	461 AA.
DC	P31394;			
DT	01-JUN-1993 (Rel. 26, Created)			
DT	01-JUN-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)			
DE	(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).			
GN	Rattus norvegicus (Rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Mistar; TISSUE=Liver;			
RX	MEDLINE=92329550; PubMed=1627650;			
RA	Okatsuji T., Maekawa K., Nawa K., Matsumoto Y.;			
RL	"The cDNA cloning and mRNA expression of rat protein C.",			
	Biochim. Biophys. Acta 1131:329-332(1992).			

CC	- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC	- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIia.
CC	- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE C-TERMINUS OF THE HEAVY CHAIN, IS STRONGLY PROMOTED BY THROMBOMODULIN.
CC	- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC	- PM: THE VITAMIN K-DEPENDENT ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM. TO ANOTHER SITE, BEYOND THE GLA DOMAIN, THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-----
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CC	-----
DR	EMBL, X64336, CAA54517.1, -.
DR	PIR, S18994, S18994.
DR	PIR, S24312, S24312.
DR	HSSP, P04070, IPCU.
DR	MEROPS, S01.218, -.
DR	InterPro, IPRO00152, Asx_hydroxyl.
DR	InterPro, IPRO01314, Chymotrypsin.
DR	InterPro, IPRO00561, EGF-like.
DR	InterPro, IPRO01881, EGF_Ca.
DR	InterPro, IPRO02383, GLA_Blood.
DR	InterPro, IPRO01254, Ser_protease_Try.
DR	InterPro, IPRO00294, Vitk_dep_GLA.
DR	Pfam, PF00008, EGF_2.
DR	Pfam, PF00089, trypsin, 1.
DR	Pfam, PF00594, gla, 1.
DR	PRINTS, PR00722, CHYMOTRYPSIN.
DR	PRINTS, PR00001, GLABLOOD.
DR	SMART, SM00179, EGF_CA, 1.
DR	SMART, SM00001, EGF_like, 1.
DR	SMART, SM00069, GLA, 1.
DR	SMART, SM00020, TRYD_Spc, 1.
DR	PROSITE, PS00010, ASX_HYDROXYL, 1.
DR	PROSITE, PS00022, EGF_1, 1.
DR	PROSITE, PS01186, EGF_2, 2.
DR	PROSITE, PS01187, EGF_CA, 1.
DR	PROSITE, PS00011, GLU_CARBOXYLATION, 1.
DR	PROSITE, PS02040, TRYPsin_DOM, 1.
DR	PROSITE, PS00134, TRYPSIN_HIS, 1.
DR	PROSITE, PS00135, TRYPSIN_SER, 1.
KW	Blood coagulation; Glycoprotein; Serine protease;
KW	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM	EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT	SIGNAL 1 32
FT	PROPEP 33 41
FT	CHAIN 42 196
FT	CHAIN 199 461
FT	PEPTIDE 212 212
FT	SITE 212 213
FT	DOMAIN 96 131
FT	DOMAIN 135 175
FT	DOMAIN 213 461
FT	MOD_RES 47 47
FT	MOD_RES 48 48
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).

RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 cDNA.";
 RL Gene 41:311-314(1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83252207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Saegawa T., Howard W.N.,
 Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 coagulation factor X: evidence for identification of residue 63 as
 beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 peptides of blood coagulation factor X. The role of the carbohydrate
 moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kanata K., Kawamoto H., Honma T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 converts prothrombin to thrombin in the presence of factor Va,
 calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM.
 CC -1- PM: N- AND O-GLYCOSYLATED.
 CC -1- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
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 CC -----
 CC EMBL, K03194; AAA52490.1; -;
 DR EMBL, M57285; AAA52421.1; -;
 DR EMBL, L29433; AAA52764.1; -;
 DR EMBL, L00390; AAA52764.1; JOINED.
 DR EMBL, L00391; AAA52764.1; JOINED.
 DR EMBL, L00392; AAA52764.1; JOINED.
 DR EMBL, L00393; AAA52764.1; JOINED.
 DR EMBL, L00394; AAA52764.1; JOINED.
 DR EMBL, L00395; AAA52764.1; JOINED.
 DR EMBL, L00396; AAA52764.1; JOINED.
 DR EMBL, M22613; AAA51984.1; -;
 DR EMBL, K01886; AAA52486.1; -;
 DR EMBL, M33297; AAA52636.1; -;
 DR PIR, A00924; EXHU.
 DR PIR, A25853; A25853.
 DR PIR, A24478; A24478.
 DR PDB, 1HCG; 08-MAY-95.
 DR PDB, 1FAK; 29-OCT-97.
 DR PDB, 1FXJ; 17-JUN-98.
 DR PDB, 1XKA; 23-MAR-99.
 DR PDB, 1XKB; 23-MAR-99.
 DR MEROPS; S01.216; -;
 DR GlycoSiteDB; P00742; -;
 DR GeneW; HGNC:3528; F10.
 DR MIM; 134530; -;
 DR MIM; 227600; -;
 DR InterPro; IPR001052; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_Blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin_1.
 DR Pfam; PF00594; gla_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_Ca_1.
 DR SMART; SM00001; EGF_like_1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; Tryp_spec_1.
 DR PROSITE; PS00010; ASX_HYDROXYL_1.
 DR PROSITE; PS00022; EGF_1_1.
 DR PROSITE; PS01186; EGF_2_2.
 DR PROSITE; PS01187; EGF_Ca_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE; PS50240; TRYPSIN_DOM_1.
 DR PROSITE; PS00134; TRYPSIN_HIS_1.
 DR PROSITE; PS00135; TRYPSIN_SER_1.
 KM Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 FT Signal; Ymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31
 FT PROPEP 32 40
 FT CHAIN 41 179
 FT CHAIN 183 488
 FT PROPEP 183 234
 FT CHAIN 235 488
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 235 488
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 59 59
 FACTOR X LIGHT CHAIN.
 FACTOR X HEAVY CHAIN.
 ACTIVATION PEPTIDE.
 ACTIVATED FACTOR XA, HEAVY CHAIN.
 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 EGF-LIKE 2.
 SERINE PROTEASE.
 GAMMA-CARBOXYGLUTAMIC ACID.
 GAMMA-CARBOXYGLUTAMIC ACID.
 GAMMA-CARBOXYGLUTAMIC ACID.
 GAMMA-CARBOXYGLUTAMIC ACID.
 GAMMA-CARBOXYGLUTAMIC ACID.

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FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 /FTID=CAR_000012.
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
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FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

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Query Match 52.1%; Score 99; DB 1; Length 488;
 Best Local Similarity 38.6%; Pred. No. 7.3e-10;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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Oy 1 ANAFLLXRLQSLRXCKXQCSFXXAEXIFKDXRTKLFMISY 44
Db 41 ANSFLFMKKGHLEKRECMERTCSYEAREVEFSDKTNEMWNY 84

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RESULT 11

FA10_RABIT STANDARD; PRT; 490 AA.

ID FA10_RABIT 019045;

DT 15-DEC-1998 (rel. 37, 'Created)

DT 15-DEC-1998 (rel. 37, 'Last sequence update)

DT 15-JUN-2002 (rel. 41, 'Last annotation update)

DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).

GN F10.

OS Oryctolagus cuniculus (Rabbit).

OC Mammalia; Eutheria; Chordata; Vertebrata; Euleleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RP [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=97256311; PubMed=9101642;

RA Pendurichi U.R.; Anderson K.D.; James H.L.;

RA "Characterization of a full-length cDNA for rabbit factor X.";

RL Thromb. Res. 85:503-514(1997).

CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that

CC converts prothrombin to thrombin in the presence of factor Va,

CC calcium and phospholipid during blood clotting.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Thr and then

CC Arg|-Ile bonds in prothrombin to form thrombin.

CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR

CC MORE DISULFIDE BONDS.

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM (BY SIMILARITY).

CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).

CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)

CC (BY SIMILARITY).

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO

CC ANOTHER SITE, BEYOND THE GLA DOMAIN.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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 or send an email to license@isb-sib.ch).

DR EMBL: AF003200; AAB62542.1; -.

DR HSSP: P00742; IHCG.

DR MEROPS: S01.216; -.

DR InterPro: IPR00152; Aex_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000742; EGF 2.

DR InterPro: IPR001881; EGF-Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Ser_protease_Try.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam: PF00008; EGF; 2.

DR Pfam: PF00089; trypsin; 1.

DR Pfam: PF00594; gla; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00001; EGF_like; 1.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; Tryp_Src; 1.

DR PROSITE: PS00010; ASK_HYDROXYL; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.

DR PROSITE: PS00240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.

KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;

KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

KW Signal; Zymogen; EGF-like domain; Repeat.

KM SIGNAL: 1 20

FT PROPEP 21 40 BY SIMILARITY.

FT CHAIN 41 180 FACTOR X LIGHT CHAIN.

FT CHAIN 184 490 FACTOR X HEAVY CHAIN.

FT PROPEP 184 232 ACTIVATION PEPTIDE.

FT CHAIN 233 490 ACTIVATION FACTOR XA, HEAVY CHAIN.

FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 125 165 EGF-LIKE 2.

FT DOMAIN 233 490 SERINE PROTEASE.

FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 47 47 SIMILARITY).

FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 54 54 SIMILARITY).

FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 59 59 SIMILARITY).

FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 60 60 SIMILARITY).

FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 65 65 SIMILARITY).

FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 66 66 SIMILARITY).

FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 69 69 SIMILARITY).

FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 72 72 SIMILARITY).

FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 75 75 SIMILARITY).

FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY

FT MOD_RES 79 79 SIMILARITY).

FT ACT_SITE 103 103 HYDROXYLATION (BY SIMILARITY).

FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.

FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.

FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.

FT DISULFID 90 101 BY SIMILARITY.

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FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 53965 MM; 3A39FA85AF2A6D11 CRC64;

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Query Match 52.1%; Score 99; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 7.3e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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OY 1 ANAFPLXLRQGSIXRXCXKXCCSFXXAEXIFPDAXRTKLFWISY 44
Db 41 ANSFLEELKGNLRECEMEICSYEALVEFEDREKTEPFMKY 84

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RESULT 12
TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RA MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF36350; AAK00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 78 PROTEIN 3.
FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).

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FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MM; 8A373E4848490B81 CRC64;

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Query Match 48.9%; Score 93; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 4e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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OY 1 ANAFPLXLRQGSIXRXCXKXCCSFXXAEXIFPDAXRTKLFWISY 44
Db 20 ANSFLEELKGNLRECEMEICSYEALVEFEDREKTEPFMKY 63

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RESULT 13
PA10 CHICK STANDARD; PRT; 475 AA.
ID PA10 CHICK
AC P25155;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor)
DE (virus activating protease) (VAP).
GN FX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorioallantoic membrane;
RA MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,
RA Ogasawara T., Nagai Y.;
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.";
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RA MEDLINE=91065352; PubMed=2174359;
RA Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.";
RL EMO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC EMBL, D00844; BAA00724.1; -.
DR HSR; S15838; S15838.
DR PSSP; P00742; IHCG.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_deg_Gla.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00068; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_HIS; 1.
DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20 OR 30; OR 31 (POTENTIAL).
FT PROPEP 21 40
FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT CHAIN 186 475 FACTOR X HEAVY CHAIN.
FT PROPEP 186 241 ACTIVATION PEPTIDE.
FT CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 168 EGF-LIKE 2.
FT DOMAIN 241 475 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.

FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 152 BY SIMILARITY.
FT DISULFID 154 167 BY SIMILARITY.
FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT DISULFID 247 252 BY SIMILARITY.
FT DISULFID 267 283 BY SIMILARITY.
FT DISULFID 366 410 BY SIMILARITY.
FT DISULFID 421 449 BY SIMILARITY.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 48.4%; Score 92; DB 1; Length 475;
Best Local Similarity 38.6%; Pred. No. 1.3e-08;
Matches 17; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXRLRQSLRXKXCCGKXCFXAXEYIFDVARTKLFWISY 44
Db 41 ANSFLEMKQGNIERECNERCSKEARAFEDNEXTEEFNNIY 84

RESULT 14
PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic cleavage product of protein C) (Blood coagulation factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014626; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGallivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6696676;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6696677;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmen N.L., Debaile L.E., Esmen C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C";
RL J. Biol. Chem. 258:5548-5553 (1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;

MODIFIER PROTEIN TO BIND CALCIUM.
IT ALSO BINDS, WITH STRONGER AFFINITY TO
GLA DOMAIN, THIS GLA-INDEPENDENT BINDING
SITE RECOGNITION OF THE
PEPTIDASE FAMILY S1.
GF-LIKE DOMAINS.

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<http://www.isb-sib.ch/>).

oxyl].
.a.
ease_Try.
_GLA.

L/L; 1.
activation; 1.
-M; 1.
S; 1.
R; 1.
asin; Serine protease;
Calcium-binding; Vitamin K; Hydroxylation;
intestinal cell; Hydrolase; Signal.
BY SIMILARITY.
BY SIMILARITY.
VITAMIN K-DEPENDENT PROTEIN C.
PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
EGF-Like 1.
EGF-Like 2.
SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.

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FT  ACT SITE 399 398 CHANGE RELAY SYSTEM.
FT DISULFID 53 58 BY SIMILARITY.
FT DISULFID 86 105 BY SIMILARITY.
FT DISULFID 95 100 BY SIMILARITY.
FT DISULFID 99 114 BY SIMILARITY.
FT DISULFID 116 125 BY SIMILARITY.
FT DISULFID 134 145 BY SIMILARITY.
FT DISULFID 141 154 BY SIMILARITY.
FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MM; D75A5F990C8F29D7 CRC64;

Query Match 44.7%; Score 85; DB 1; Length 458;
Best Local Similarity 40.9%; Pred. No. 2.1e-07;
Matches 18; Conservative 3; Mismatches 23; Indels 0; Gaps 0

Qy 1 ANAFLXLRQGSILRXCKXXQCSFXXAEKIFPDARTKLFWISY 44
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 37 ANSFLELRPSSLEREVCVCDLEAEKIFQSVDDTLAFWYKY 80

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10gln28g1u
Sequence: 1 ANAFXXLRQSLXRCCKX.....XXAEXIFDAXRTLFMISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_proteic:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	159	83.7	701	4	Q96PQ8	Q96PQ8 homo sapien
2	114	60.0	446	11	Q61109	Q61109 mus musculu
3	102	53.7	460	11	Q91WN8	Q91WN8 mus musculu
4	96	50.5	460	11	Q99PC6	Q99PC6 mus musculu
5	93	48.9	482	11	Q63207	Q63207 rattus norv
6	92	48.4	456	6	Q9TTR0	Q9TTR0 canis famli
7	91	47.9	469	6	Q9GMD9	Q9GMD9 ornithorhyn
8	91	47.9	481	11	Q54740	Q54740 mus musculu
9	91	47.9	481	11	Q99L32	Q99L32 mus musculu
10	91	47.9	481	11	Q88947	Q88947 mus musculu
11	85	44.7	100	4	Q15253	Q15253 homo sapien
12	83	43.7	456	4	Q14316	Q14316 homo sapien
13	83	43.7	461	6	Q95ND7	Q95ND7 pan troglod
14	83	43.7	461	6	Q95ND7	Q95ND7 pan troglod
15	82	43.2	49	6	Q95ME8	Q95ME8 bos taurus
16	76	40.0	179	4	Q8TAS3	Q8TAS3 homo sapien

17	76	40.0	198	11	Q8R182	Q8R182 mus musculu
18	75	39.5	138	6	Q28994	Q28994 sus scrofa
19	70	36.8	433	13	Q90YK1	Q90YK1 brachydanio
20	70	36.8	648	6	Q29094	Q29094 sus scrofa
21	67	35.3	399	11	Q9CQW3	Q9CQW3 mus musculu
22	65	34.2	98	13	P82807	P82807 notechis sc
23	65	34.2	650	4	Q9NSD0	Q9NSD0 homo sapien
24	65	34.2	650	4	Q16519	Q16519 homo sapien
25	63	33.2	542	5	Q9PTW7	Q9PTW7 struthio ca
26	60.5	31.8	608	13	Q8T613	Q8T613 halocynthia
27	60	31.6	607	13	Q91001	Q91001 gallus gall
28	58.5	30.8	431	10	Q94EY5	Q94EY5 arabisdopsis
29	58.5	30.8	492	10	Q9SMU7	Q9SMU7 cicor artet
30	58.5	30.8	543	10	Q9MB23	Q9MB23 arabisdopsis
31	58.5	30.8	576	10	Q9C9U4	Q9C9U4 arabisdopsis
32	58.5	30.8	589	10	Q9LMS2	Q9LMS2 arabisdopsis
33	57.5	30.3	196	10	Q04284	Q04284 selaginella
34	56.5	29.7	459	10	Q9SE22	Q9SE22 oryza sativ
35	56	29.5	673	11	Q61592	Q61592 mus musculu
36	56	29.5	674	11	Q99K57	Q99K57 mus musculu
37	55.5	29.2	506	10	Q9SPF0	Q9SPF0 oryza sativ
38	55.5	29.2	506	10	Q9SE23	Q9SE23 oryza sativ
39	55.5	29.2	567	10	Q8W4J2	Q8W4J2 arabisdopsis
40	55	28.9	25	11	Q9QVH6	Q9QVH6 rattus sp.
41	54.5	28.7	510	10	Q9MB22	Q9MB22 arabisdopsis
42	54.5	28.7	619	10	Q9LV37	Q9LV37 arabisdopsis
43	54	28.4	674	11	Q63772	Q63772 rattus sp.
44	54	28.4	678	4	Q14393	Q14393 homo sapien
45	52.5	27.6	588	10	Q9LM33	Q9LM33 arabisdopsis

ALIGNMENTS

RESULT 1
ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant Immunofugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR01881; EGF-Ca.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF-Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CBB42CC992F CRC64;

Query Match 83.7%; Score 155; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 1.1e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXKXGCSFXXAEXIFKDXRTKLFWISY 44
DB 61 ANAFLEELRPGSLRECKEKGCSFEERAREIFKDAERTKLFWISY 104

RESULT 2

061109 PRELIMINARY; PRT; 446 AA.

AC 061109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96376538; PubMed=8701412;
RA Iduogile E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
CC Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDDA6870 CRC64;

Query Match 60.0%; Score 114; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.5e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXKXGCSFXXAEXIFKDXRTKLFWISY 44
DB 42 ANSLEELWPGSLRECKNEGCSFEERAREIFKSPEETKQFWIV 85

RESULT 3

091WN8 PRELIMINARY; PRT; 460 AA.

AC 091WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 53.7%; Score 102; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 2.6e-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXKXGCSFXXAEXIFKDXRTKLFWISY 44
DB 42 ANSFLBMRPGSLRECKMEICDFEERAREIFQVVEDTLAFWIKY 85

RESULT 4

099PC6 PRELIMINARY; PRT; 460 AA.

AC 099PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
KW Korf I.;

RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MCD; MG1.97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 50.5%; Score 96; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 3.4e-09;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRQGLXRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
Db 42 ANSFLEMRPGSLERECMEICDLBEAQEIFQNVEDTLAFWIKY 85

RESULT 5
ID Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; Pubmed=8578539;
RA Stanton C., Ross R.P., Hutton S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY
DR EMBL; X79807; CAAS6202.1; -.
DR HSSP; P00742; 1XRA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 1.3e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRQGLXRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
Db 41 ANSFEEIKKGNLERECVEICISFEAREVFDENKTEFMNKY 84

RESULT 6
ID Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein C precursor.
CN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; Pubmed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY
DR EMBL; AJ001979; CAAS0126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

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DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; tryp_spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192
FT CHAIN 133 194
FT CHAIN 195 456
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match
Best Local Similarity 48.4%; Score 92; DB 6; Length 456;
Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLXKXCKXQGSFXXAEXIFKAKRTKLFWISY 44
Db 43 ANSFLERIRAGSLERECMERICDFEEKEIFQVNDTLAYWSKY 86

RESULT 7
Q9GMD9 PRELIMINARY; PRT; 469 AA.
AC Q9GMD9;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OC NCBI_TaxId=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=1132153;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
RT monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL; AF275654; AAC00453.1; -.
CC HSSP; P00742; 1XKA.
CC MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_Ca.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
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DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; tryp_spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match
Best Local Similarity 47.9%; Score 91; DB 6; Length 469;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLXKXCKXQGSFXXAEXIFKAKRTKLFWISY 44
Db 41 ANSFLERIRAGSLERECMERICDFEEKEIFQVNDTLAYWSKY 84

RESULT 8
O54740 PRELIMINARY; PRT; 481 AA.
AC O54740;
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR FALD.
OS Mus musculus (Mouse).
OC Plasmid pBluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RX MEDLINE=96454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL; AF222677; CA010933.1; -.
CC HSSP; P00742; 1XKA.
CC MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; tryp_spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00134; TRYPSIN_DOM; 1.
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DR PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KM Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E5F9D97AE CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08; Mismatches 20; Indels 0; Gaps 0;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLKRXKXCCXQCSFXXAEXIFPDARTKLFMISY 44
Db 41 ANSFEEFKGNLRECHMEICSYEEVREIFEDDEKTEKYEWTKY 84

RESULT 9
ID 099132 PRELIMINARY; PRT; 481 AA.
AC 099132;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
Cy 1 ANAFIXLRGSLKRXKXCCXQCSFXXAEXIFPDARTKLFMISY 44
Db 41 ANSFEEFKGNLRECHMEICSYEEVREIFEDDEKTEKYEWTKY 84

RESULT 10
ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=96347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL; AF087644; AAC6345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; BAC09D5E5F9D271E CRC64;

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Query Match          47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 41 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 84

RESULT 11
ID 015253 PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N. Y. Acad. Sci. 485:73-79(1996).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PPI.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GSA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Signal.
FT SIGNAL. 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD055D0174E1FEFE CRC64;

Query Match          44.7%; Score 85; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 7.8e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 44 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 87

RESULT 12
ID 014316 PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas disease, HEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Retsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

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RA Brict E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

QY 10 QGSLXRXCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 52 QGSLXRXCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 86

RESULT 13
ID 095ND7 PRELIMINARY; PRT; 461 AA.
AC 095ND7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RT Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.

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DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
KM SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;
SQ
Query Match 43.7%; Score 83; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 8.7e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 10 QGSLRXCKXKQCSFPXAEKIFKDXRTKLFWISY 44
Db 57 QGNLERCEKCKSFEEAREVFENTERTTEFWKQY 91

RESULT 14
OQ5ND6 PRELIMINARY; PRT; 461 AA.
AC OQ5ND6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Saita Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
KM SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;
SQ
Query Match 43.7%; Score 83; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 8.7e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 10 QGSLRXCKXKQCSFPXAEKIFKDXRTKLFWISY 44
Db 57 QGNLERCEKCKSFEEAREVFENTERTTEFWKQY 91

RESULT 15
OQ5ME8 PRELIMINARY; PRT; 49 AA.
AC OQ5ME8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amarel E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF394598; AAK77556.1; -.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; G1a; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 43.2%; Score 82; DB 6; Length 49;
Best Local Similarity 40.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Oy 10 QGSLRXCKXKQCSFPXAEKIFKDXRTKLFWISY 44
Db 14 RGNLERCEKCKSFEEAREVFENTERTTEFWKQY 48
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Search completed: March 19, 2003, 15:13:27
Job time : 59.3125 secs

AGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLN28GLU

Perfect score: 190

Sequence: 1 ANAFLXLRQGSIXRXCCKX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*

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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	85.3	44	3	US-08-955-636-26
2	161	84.7	44	3	US-08-955-636-30
3	160	84.2	44	3	US-08-955-636-27
4	159	83.7	44	3	US-08-955-636-3
5	159	83.7	406	1	US-08-293-778-24
6	159	83.7	406	1	US-08-295-411-5
7	159	83.7	406	1	US-08-955-471-5
8	159	83.7	406	5	PCT-US92-10242-5
9	159	83.7	444	1	US-08-475-845-2
10	159	83.7	444	2	US-08-327-680-2
11	159	83.7	444	2	US-08-660-289-2
12	159	83.7	444	2	US-08-537-807-2
13	159	83.7	444	2	US-08-871-003-2
14	159	83.7	444	2	US-08-464-233-2
15	159	83.7	444	4	US-09-189-607-2
16	159	83.7	444	4	US-09-378-907-2
17	159	83.7	444	5	PCT-US94-05779-2
18	159	83.7	466	1	US-07-882-202A-4
19	159	83.7	466	1	US-08-021-615A-4
20	159	83.7	466	1	US-08-321-777-4
21	159	83.7	466	4	US-09-009-217-14
22	159	83.7	466	4	US-09-009-656-14
23	159	83.7	466	5	PCT-US93-04493-4
24	156	82.1	44	3	US-08-955-636-28
25	153	80.5	44	3	US-08-955-636-29
26	144	75.8	41	1	US-08-229-280-4
27	123	64.7	44	3	US-08-955-636-4

28	108	56.8	139	1	US-08-330-978-2	Sequence 2, Appli
29	108	56.8	139	1	US-08-474-042-2	Sequence 2, Appli
30	108	56.8	139	1	US-08-484-558-2	Sequence 2, Appli
31	108	56.8	139	1	US-08-774-592-2	Sequence 2, Appli
32	108	56.8	437	1	US-08-487-037-2	Sequence 2, Appli
33	108	56.8	437	1	US-08-487-037-3	Sequence 3, Appli
34	108	56.8	448	1	US-08-487-037-1	Sequence 1, Appli
35	102	53.7	44	3	US-08-955-636-18	Sequence 18, Appli
36	102	53.7	487	2	US-08-469-486-53	Sequence 53, Appli
37	102	53.7	487	2	US-08-469-486-53	Sequence 53, Appli
38	102	53.7	487	2	US-08-469-486-53	Sequence 53, Appli
39	102	53.7	487	2	US-08-469-486-53	Sequence 53, Appli
40	101	53.2	44	3	US-08-955-636-24	Sequence 24, Appli
41	99	52.1	448	1	US-08-295-411-3	Sequence 3, Appli
42	99	52.1	448	2	US-08-955-471-3	Sequence 3, Appli
43	99	52.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
44	99	52.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
45	98	51.6	44	3	US-08-955-636-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-955-636-26
Sequence 26, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0) ..(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 85.3%; Score 162; DB 3; Length 44;
Best local Similarity 95.5%; Pred. No. 3.9e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXLRQGSIXRXCCKXCFXAXEIRFKDXRTKLFWISY 44
DB 1 ANAFLXLRQGSIXRXCCKXCFXAXEIRFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: MOD.RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 84.7%; Score 161; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.7e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44
DB 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 3
US-08-955-636-27

Sequence 27, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsaestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955, 636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD.RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-27

Query Match 84.2%; Score 160; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 8.4e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44
DB 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 4
US-08-955-636-3

Sequence 3, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsaestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955, 636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD.RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-3

Query Match 83.7%; Score 159; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.2e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44
DB 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 5
US-08-293-778-24

Sequence 24, Application US/08293778
Patent No. 5580560

GENERAL INFORMATION:

APPLICANT: Nicolaesen, Else M.

APPLICANT: Bjorn, Soren E.

APPLICANT: Wiberg, Finn C.

TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,778

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509

FILING DATE:

APPLICATION NUMBER: DK 3235/87

FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/434,149

FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK88/00103

FILING DATE: 24-JUN-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/898,248

FILING DATE: 12-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Agtib, Cheryl H.

REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3129,224-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-867-0298

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 406 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-293-778-24

Query Match 83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44
DB 1 ANAFLXXLRQGSIXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 6
US-08-295-411-5


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; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-6312
; TELEFAX: 619-554-2937
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match      83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRQGSILKRXCKXQCSFYXAEIIFDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLERCKEEOCSFEAREIIFDAXRTKLFWISY 44
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RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
```

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; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5

Query Match      83.7%; Score 159; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRQGSILKRXCKXQCSFYXAEIIFDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLERCKEEOCSFEAREIIFDAXRTKLFWISY 44
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RESULT 8
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
```

```

; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note="Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note="Factor VII Heavy Chain"
; PCT-US92-10242-5

Query Match      83.7%; Score 159; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1,2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
Db 1 ANAFLRLRPGSLERCKEQCSFEARLIFKDAERTKLFWISY 44

RESULT 9
US-08-475-845-2
; Sequence 2, Application US/08475845
; Patent No. 5788965
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/475,845
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-845-2

Query Match      83.7%; Score 159; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1,3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
Db 39 ANAFLRLRPGSLERCKEQCSFEARLIFKDAERTKLFWISY 82

RESULT 10
US-08-327-690-2
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920

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FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFIXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 11
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFIXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 12
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFIXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 13
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.

APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRQSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEQCSFEERAREIFKDAERTKLFWISY 82

RESULT 14
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 83.7%; Score 159; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRQSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEQCSFEERAREIFKDAERTKLFWISY 82

RESULT 15
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/662,920
 ; FILING DATE: 28-FEB-1991
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-8-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-467-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 444 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-189-607-2

Query Match 83.7%; Score 159; DB 4; Length 444;
 Best Local Similarity 72.7%; Pred. No. 1.3e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRLQGSILRXCKXQCSFYXAXEYIFDAXRTKLFWISY 44
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 Db 39 ANAFLELRPGSLERECKEQCSFEARERIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:11
 Job time : 15.75 secs

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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10GLN28GLU
Perfect score: 190
Sequence: 1 ANAFLLXLRPGSLXKXCKXK.....XXAEXIFDAXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Published Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCFUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	ID	Description
1	159	83.7	406	US-10-109-498-1	Sequence 1, Appli
2	101	53.2	419	US-10-182-263-6	Sequence 6, Appli
3	96	50.5	419	US-10-182-263-3	Sequence 3, Appli
4	96	50.5	419	US-10-182-263-4	Sequence 4, Appli
5	96	50.5	419	US-10-182-263-5	Sequence 5, Appli
6	85	44.7	419	US-10-182-263-1	Sequence 1, Appli
7	85	44.7	419	US-09-978-917A-4	Sequence 4, Appli
8	85	44.7	461	US-10-182-263-2	Sequence 2, Appli
9	85	44.7	461	US-09-978-917A-2	Sequence 2, Appli
10	83	43.7	415	US-09-118-748-2	Sequence 2, Appli
11	83	43.7	461	US-10-132-829-5	Sequence 5, Appli
12	83	43.7	461	US-09-884-901-3	Sequence 3, Appli
13	69.5	36.6	96	US-09-759-130B-313	Sequence 313, App
14	69.5	36.6	209	US-09-759-130B-112	Sequence 312, App
15	69.5	36.6	226	US-09-759-130B-310	Sequence 310, App
16	54.5	28.7	98	US-09-759-130B-356	Sequence 356, App
17	54.5	28.7	208	US-09-759-130B-355	Sequence 355, App
18	54.5	28.7	225	US-09-759-130B-353	Sequence 353, App
19	43	22.6	88	US-09-811-284-194	Sequence 194, App

20	43	22.6	273	9	US-09-764-868-968	Sequence 968, App
21	43	22.6	1266	9	US-09-931-969A-2	Sequence 2, Appli
22	43	22.6	1266	9	US-10-079-699-2	Sequence 2, Appli
23	43	22.6	1266	10	US-09-757-781-63	Sequence 63, Appli
24	43	22.6	1356	10	US-09-757-781-2	Sequence 2, Appli
25	42	22.1	608	10	US-09-908-664-5	Sequence 5, Appli
26	42	22.1	729	9	US-10-145-366-11	Sequence 11, Appli
27	42	22.1	1258	10	US-09-922-543-1	Sequence 1, Appli
28	42	22.1	1274	10	US-09-746-491-12	Sequence 12, Appli
29	41.5	21.8	440	9	US-09-910-186A-8	Sequence 8, Appli
30	41	21.6	447	10	US-09-815-242-13490	Sequence 13490, A
31	41	21.6	447	10	US-09-815-242-13612	Sequence 13612, A
32	41	21.6	447	10	US-09-735-564-2	Sequence 2, Appli
33	40.5	21.3	1149	10	US-09-969-528-5	Sequence 5, Appli
34	40	21.1	744	10	US-09-862-179A-1	Sequence 1, Appli
35	40	21.1	1337	10	US-09-757-781-62	Sequence 62, Appli
36	39	20.5	52	9	US-09-796-692-2179	Sequence 2179, App
37	39	20.5	52	9	US-09-796-692-2370	Sequence 2370, App
38	39	20.5	347	10	US-09-780-053-4	Sequence 4, Appli
39	39	20.5	730	9	US-10-145-396-12	Sequence 12, Appli
40	39	20.5	730	10	US-09-780-053-2	Sequence 2, Appli
41	39	20.5	873	9	US-10-200-154-2	Sequence 2, Appli
42	39	20.5	873	10	US-09-954-043-2	Sequence 2, Appli
43	38.5	20.3	49	10	US-09-764-864-1054	Sequence 1054, App
44	38.5	20.3	316	10	US-09-815-242-11911	Sequence 11911, A
45	38.5	20.3	348	10	US-09-982-610-18	Sequence 18, Appli

ALIGNMENTS

```

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      83.7%; Score 159; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 1.1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ANAFLLXLRPGSLXKXCKXKOCSEFXAXEIFDAXRTKLFWISY 44
DB 1 ANAFLLXLRPGSLXKXCKXKOCSEFXAXEIFDAXRTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

```

```
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ PRIOR FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          53.2%; Score 101; DB 9; Length 419;
Best Local Similarity 51.2%; Pred. No. 3.3e-10;
Matches 21; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCKXXQCSFXXAEXIFKDAKRTKLFW 41
DB 1 ANSFLELRHGSLEKCEIEICDFEAKKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-3
/ Sequence 3, Application US/10182263
/ Publication No. US20030022354A1
/ GENERAL INFORMATION:
/ APPLICANT: Geriltz, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ CURRENT FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.6e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCKXXQCSFXXAEXIFKDAKRTKLFW 41
DB 1 ANSFLELRHGSLEKCEIEICDFEAKKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-4
/ Sequence 4, Application US/10182263
/ Publication No. US20030022354A1
/ GENERAL INFORMATION:
/ APPLICANT: Geriltz, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ CURRENT FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
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/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.6e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCKXXQCSFXXAEXIFKDAKRTKLFW 41
DB 1 ANSFLELRHGSLEKCEIEICDFEAKKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-5
/ Sequence 5, Application US/10182263
/ Publication No. US20030022354A1
/ GENERAL INFORMATION:
/ APPLICANT: Geriltz, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ CURRENT FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.6e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCKXXQCSFXXAEXIFKDAKRTKLFW 41
DB 1 ANSFLELRHGSLEKCEIEICDFEAKKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-1
/ Sequence 1, Application US/10182263
/ Publication No. US20030022354A1
/ GENERAL INFORMATION:
/ APPLICANT: Geriltz, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C DERIVATIVES
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US/10/182,263
/ CURRENT FILING DATE: 2002-07-22
/ PRIOR APPLICATION NUMBER: 60/181948
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/189199
/ PRIOR FILING DATE: 2000-03-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 419
/ TYPE: PRT
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ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.5e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAXEYFKDAXRTKLFW 41
Db 1 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 41

RESULT 7
US-09-978-917A-4

Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.5e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAXEYFKDAXRTKLFW 41
Db 1 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 41

RESULT 8
US-10-182-263-2

Sequence 2, Application US/10182263
Publication No. US20030022354A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 2.8e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAXEYFKDAXRTKLFW 41
Db 43 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT FILING DATE: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 2.8e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAXEYFKDAXRTKLFW 41
Db 43 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 83

RESULT 10
US-09-118-748-2

Sequence 2, Application US/09118748A
Patent No. US20020031799A1

GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
TITLE OF INVENTION: Activity
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118,748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT

ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 43.7%; Score 83; DB 10; Length 415;
Best Local Similarity 42.9%; Pred. No. 5.8e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLRXCKXKXQCSFYXAXEYFKDAXRTKLFWISY 44
Db 11 QGNLERECMEKCSFEARVEVENTERTTTEFWKQY 45

RESULT 11
US-10-132-829-5

Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
TITLE OF INVENTION: with vesicle vector
FILE REFERENCE: 6627-P41170

```

; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          43.7%; Score 83; DB 9; Length 461;
Best Local Similarity 42.9%; Pred. No. 6.5e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXKQCSFXXAEXIFDAXRTKLFWMISY 44
DB 57 QGNLRECEMEKCSFPEARVFTERTTTFWKOY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17386
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-901-3

Query Match          43.7%; Score 83; DB 10; Length 461;
Best Local Similarity 42.9%; Pred. No. 6.5e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXKQCSFXXAEXIFDAXRTKLFWMISY 44
DB 57 QGNLRECEMEKCSFPEARVFTERTTTFWKOY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          36.6%; Score 69.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 3.3e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRQGSIXRXCKXKQCSFXXAEXIFDAXRTKLFWMISY 44
DB 36 NRPDELFTPPGNLRECEMEKCSFPEARVFTERTTTFWKOY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-1308-312

Query Match 36.6%; Score 69.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 7.6e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

OY 2 NAF-LXXLRQSLXKXCKXOCFFXXAEXIFKDXRTKLFWISY 44
DB 36 NRPDLFTPGNLERECNEBELCNVEAREIFVDEKTIATFMOEY 79

RESULT 15

US-09-759-1308-310
Sequence 310, Application US/09759130B
Publication No. US2003002279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirsit, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Meyers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MP100-5350M1M
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 310
LENGTH: 226
TYPE: PRT

ORGANISM: Homo sapiens
US-09-759-1308-310

Query Match 36.6%; Score 69.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 8.3e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

OY 2 NAF-LXXLRQSLXKXCKXOCFFXXAEXIFKDXRTKLFWISY 44
DB 53 NRPDLFTPGNLERECNEBELCNVEAREIFVDEKTIATFMOEY 96

Search completed: March 20, 2003, 13:30:08
Job time : 10.375 secs

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